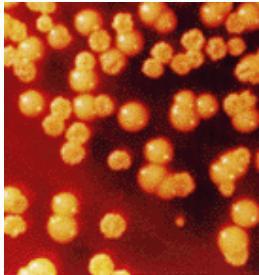


24 Nov 1999

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Phenotypic switching in the yeast *Candida albicans* results in the changed appearance of colonies grown on solid medium. But what is occurring at the molecular level?

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How *Candida albicans* switches phenotype - and back again

Among the many bugs that live in the mouth and digestive tract is the yeast *Candida albicans*, which under normal circumstances lives in 80% of the human population with no harmful effects. However, overgrowth results in thrush, a condition often observed in immunocompromised individuals such as HIV-positive patients. Candidiasis also occurs in the blood and in the genital tract. To infect host tissue, the usual unicellular yeast-like form of *C. albicans* reacts to environmental cues and switches into an invasive, multicellular filamentous form. This switching between two cell-types is known as dimorphism.

In a process that superficially resembles dimorphism, *C. albicans* undergoes a process called "phenotypic switching", in which different cellular morphologies are generated spontaneously. One of the classically studied strains that undergoes phenotypic switching is WO-1, which consists of two phases - one that grows as smooth white colonies and one that is rod-like and grows as flat gray colonies. The other strain known to undergo switching is 3153A; this strain produces at least seven different colony morphologies. In both the WO-1 and 3153A strains, the different phases convert spontaneously to the other(s) at a low frequency. The switching is reversible, and colony type can be inherited from one generation to another. While several genes that are expressed differently in different colony morphologies have been identified, some recent efforts have focussed on what might be controlling these changes. Further, whether there is a potential molecular link between dimorphism and phenotypic switching is a tantalizing question.

In the 3153A strain, a gene called *SIR2* (for silent information regulator) has been found that seems to be important for phenotypic switching. *SIR2* was originally found in *Saccharomyces cerevisiae* (brewer's yeast), where it is involved in chromosomal silencing - a form of transcriptional regulation in which regions of the genome are reversibly inactivated by changes in chromatin structure (chromatin is the complex of DNA and proteins that make chromosomes). In yeast, genes involved in the control of mating type are found in these silent regions, and *SIR2* represses their expression by maintaining a silent-competent chromatin structure in this region. The discovery of a *C. albicans* *SIR2* that is implicated in phenotypic switching suggests that it too has silent regions controlled by *SIR2*, in which the phenotype-specific genes may perhaps reside.

Another potential regulatory molecule is Efg1p, a transcription factor found in the WO-1 strain that regulates dimorphism, and more recently has been suggested to help regulate phenotypic switching. Efg1p is expressed only in the white and not in the gray

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cell-type, and overexpression of Efg1p in the gray form causes a rapid conversion to the white form.

So far there are few data that says that dimorphism and phenotypic switching use common molecular components. However, it is not inconceivable that phenotypic switching may occur in response to some change in the environment as well as being a spontaneous event. How SIR2 itself is regulated in *S. cerevisiae* may yet provide clues as to the switching mechanisms of *C. albicans*.

Comments?

Questions?

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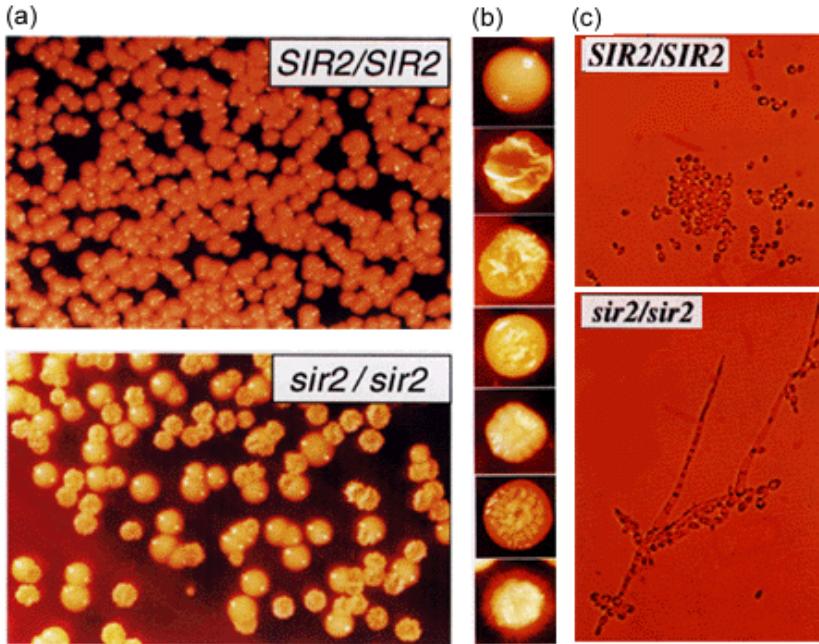
[Overview](#)[BLAST page](#)[Statistics course](#)How *Candida albicans* switches phenotype - and back again

Figure 1. Phenotypic switching in the yeast *Candida albicans* can be controlled by a *SIR2* gene. (a) Yeast colonies that are homozygous positive for the *SIR2* gene (*SIR2/SIR2*) have a uniform colony morphology, while those that lack completely *SIR2* (homozygous negative - *sir2/sir2*) have variant colony morphologies. (b) Several different colony types are possible for cells of the *sir2/sir2* phenotype. Many of the seven colony types shown here can arise from a single colony of one of the other morphologies, indicating that the phenotypic switching is heritable. (c) Filamentous growth is enhanced for *sir2/sir2* cells over *SIR2/SIR2*, which suggests that there may be common ground between the mechanisms of phenotypic switching and dimorphism in *Candida albicans*.

(Reproduced with permission from: Perez-Martin, J., Uria, J.A. and Johnson, A.D. (1999) Phenotypic switching in *Candida albicans* is controlled by a *SIR2* gene. *EMBO J.* 18, 2580-2592.)



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2 : [Baur AS, et al.](#) Related Articles
Frequent methylation silencing of p15(INK4b) (MTS2) and p16(INK4a) (MTS1) in B-cell and T-cell lymphomas.
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3 : [Di Ianni M, et al.](#) Related Articles
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4 : [Sherman JM, et al.](#) Related Articles
The conserved core of a human SIR2 homologue functions in yeast silencing.
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5 : [Wade PA, et al.](#) Related Articles
Mi-2 complex couples DNA methylation to chromatin remodelling and histone deacetylation.
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6 : [Ng HH, et al.](#) Related Articles
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7 : [Fujita N, et al.](#) Related Articles
Methylation-mediated transcriptional silencing in euchromatin by methyl-CpG binding protein MBD1 isoforms.
Mol Cell Biol. 1999 Sep;19(9):6415-26.
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8 : [Andres ME, et al.](#) Related Articles, Protein, Nucleotide
CoREST: a functional corepressor required for regulation of neural-specific gene expression.
Proc Natl Acad Sci U S A. 1999 Aug 17;96(17):9873-8.
PMID: 10449787; UI: 99380612

9 : [Rossi C, et al.](#) Related Articles
Transiently transfected and stably integrated HIV-1 LTR responds differentially to the silencing activity of the Kruppel-associated box (KRAB) transcriptional repressor domain.
J Med Virol. 1999 Jul;58(3):264-72.
PMID: 10447422; UI: 99314993

10 : [Zhang Y, et al.](#) Related Articles, Protein, Nucleotide
Analysis of the NuRD subunits reveals a histone deacetylase core complex and a connection with DNA methylation.
Genes Dev. 1999 Aug 1;13(15):1924-35.
PMID: 10444591; UI: 99375308

11 : [Iizuka M, et al.](#) Related Articles, Protein, Nucleotide
Histone acetyltransferase HBO1 interacts with the ORC1 subunit of the human initiator protein.
J Biol Chem. 1999 Aug 13;274(33):23027-34.
PMID: 10438470; UI: 99367424

12 : [Kohno T, et al.](#) Related Articles

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Carcinogenesis. 1999 Aug;20(8):1403-10. Review.
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13 : [Algar EM, et al.](#)

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14 : [Lam WW, et al.](#)

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Analysis of germline CDKN1C (p57KIP2) mutations in familial and sporadic Beckwith-Wiedemann syndrome (BWS) provides a novel genotype-phenotype correlation.
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15 : [Kawano S, et al.](#)

Related Articles

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16 : [Corn PG, et al.](#)

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17 : [Prakash A, et al.](#)

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18 : [White PJ, et al.](#)

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19 : [Wong DJ, et al.](#)

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20 : [Forsberg EC, et al.](#)

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The 'Related Articles' function found a paper that describes the cloning of the human gene similar to SIR2. This paper has nucleotide and protein sequences associated with it.

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Mol Biol Cell. 1999 Sep;10(9):3045-59.
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2 : Smith JS, et al. Related Articles
Distribution of a limited Sir2 protein pool regulates the strength of yeast rDNA silencing and is modulated by Sir4p.
Genetics. 1998 Jul;149(3):1205-19.
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3 : Afshar G, et al. Related Articles, Protein, Nucleotide
Characterization of a human gene with sequence homology to *Saccharomyces cerevisiae* SIR2.
Gene. 1999 Jun 24;234(1):161-8.
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4 : Smith JS, et al. Related Articles
A genetic screen for ribosomal DNA silencing defects identifies multiple DNA replication and chromatin-modulating factors.
Mol Cell Biol. 1999 Apr;19(4):3184-97.
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5 : Straight AF, et al. Related Articles
Net1, a Sir2-associated nucleolar protein required for rDNA silencing and nucleolar integrity.
Cell. 1999 Apr 16;97(2):245-56.
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6 : Fritze CE, et al. Related Articles
Direct evidence for SIR2 modulation of chromatin structure in yeast rDNA.
EMBO J. 1997 Nov 3;16(21):6495-509.
PMID: 9351831; UI: 98062997

7 : Brachmann CB, et al. Related Articles, Protein
The SIR2 gene family, conserved from bacteria to humans, functions in silencing, cell cycle progression, and chromosome stability.
Genes Dev. 1995 Dec 1;9(23):2888-902.
PMID: 7498786; UI: 96101589

8 : Astrom SU, et al. Related Articles, Protein, Nucleotide
Theme and variation among silencing proteins in *Saccharomyces cerevisiae* and *Kluyveromyces lactis*.
Genetics. 1998 Mar;148(3):1021-9.
PMID: 9539421; UI: 98198828

9 : Gotta M, et al. Related Articles
Localization of Sir2p: the nucleolus as a compartment for silent information regulators.
EMBO J. 1997 Jun 2;16(11):3243-55.
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10 : Kamakaka RT, et al. Related Articles
Sir- and silencer-independent disruption of silencing in *Saccharomyces* by Sas10p.
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A deubiquitinating enzyme interacts with SIR4 and regulates silencing in *S. cerevisiae*.
Cell. 1996 Aug 23;86(4):667-77.
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- 14 : [Holmes SG, et al.](#) Related Articles
Hyperactivation of the silencing proteins, Sir2p and Sir3p, causes chromosome loss.
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- 15 : [Gasser SM, et al.](#) Related Articles
Nuclear organization and silencing: trafficking of Sir proteins.
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- 16 : [Gotta M, et al.](#) Related Articles
Functional characterization of the N terminus of Sir3p.
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Silent chromatin in yeast: an orchestrated medley featuring Sir3p.
Bioessays. 1998 Jan;20(1):30-40. Review.
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This is the query page for a BLAST search. The sequence of *Candida albicans* SIR2 is entered in the textbox below. The database to be searched can be selected from the following pull-down menu, as can the format that the sequence is submitted in. Click on the "Submit Query" button below the textbox to find similar sequences to this query in the database.

Database

The amino acid query sequence is [filtered](#) for low complexity regions by default.

Enter here your **amino acid sequence** as

```
DNLEQR GLKSEKLVQCHGSF K
KCVSCQGIFAGEKEIYNHIRRKQVPRCAICWKNTKQAPIHFGAIKPT
ITFFGEDLPERFHLMKDQLQQID
LFLVIGTSLKVEPVASIIERVPYKVPKILINKDPIPNRGFNLQLLG
LCDDAVSYLCKCLKWDIPHADFNN
NDELKLSKLKNGDWEIVNKSTSTKK
```

Please read about [FASTA](#) format description

The options below are for advanced users. In this example, the number of descriptions has been set to 100, with 50 alignments returned. If no parameters are changed or selected, then BLAST is run in default mode.

Advanced options for the BLAST server:

Expect Filter NCBI-gi Graphical Overview

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Expect value for inclusion in PSI-BLAST iteration 1

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Query= gi|3005095|gb|AAC09304.1| SIR2 (515 letters) **Database:** Non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR 422,855 sequences; 129,676,735 total letters

Below are the results from a PSI-BLAST ([see Altschul et al., 1997](#)) search of the non-redundant database using *Candida albicans* SIR2 as the query sequence.

The E value is a statistical measure of likelihood that the sequences listed below are truly similar to the query, rather than found by chance alone. The lower the E value, the greater the confidence that the protein found is a biologically significant match.

E-value threshold for inclusion in PSI-Blast iteration 1: 0.001

E-value threshold for inclusion in PSI-Blast iteration 2:

PSI-BLAST constructs a similarity matrix from the significant hits found in a BLAST search and uses this matrix to search the database in a second round of BLASTing. Each round of PSI-BLAST that uses the matrix to search the database is called an iteration.

[Distribution of 51 Blast Hits on the Query Sequence](#)

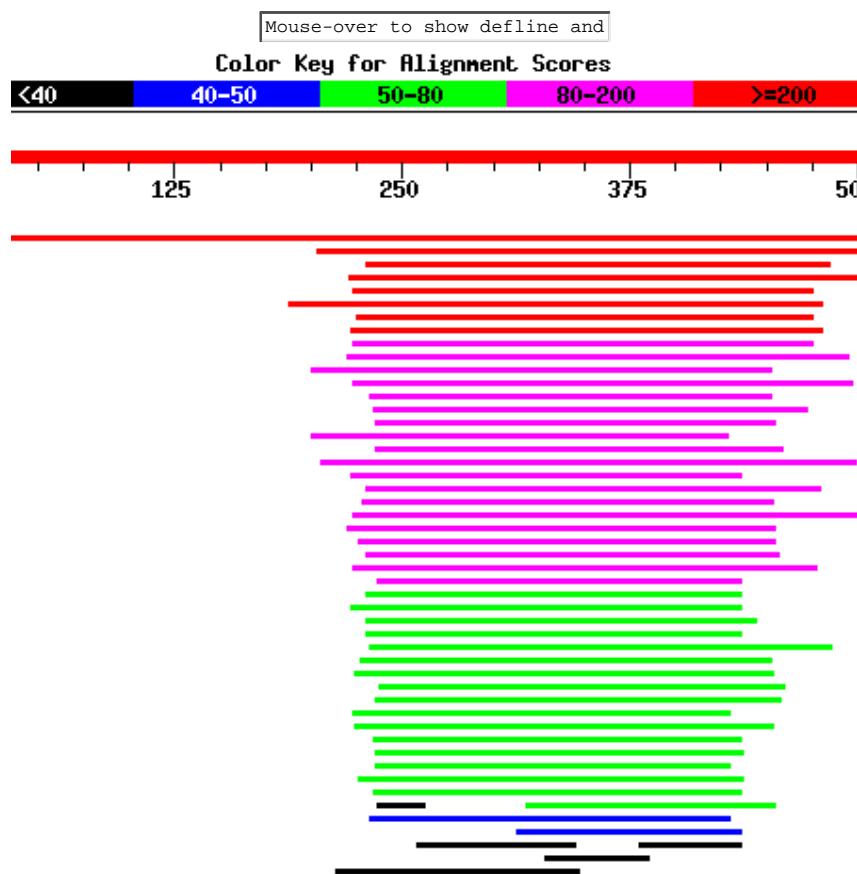


Figure legend

The above summary of the BLAST results represents proteins that match the query sequence as colored bars, with the most similar hit uppermost and appearing in red. Pink, green, blue and black bars follow, representing proteins in decreasing order of similarity. Hatched areas indicate a gap in similarity i.e., two or more distinct regions of similarity were found within the same protein hit. Moving the mouse over the bars will display the name of the matching protein found in the textbox above.

Click [here](#) to view alignments.
 Click [here](#) to see the analysis of this BLAST result.

About the alignments

The match with the top score is to itself (reassuringly) - the lower the e-value or the higher the score, the higher the chance that the similarity is biologically relevant. Clicking on the scores will take you to the alignments for each of the top ten hits (as requested in our query). Clicking on the ID numbers on the left will display the sequence record at the NCBI site.

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or

Click [here](#) to see the analysis of this BLAST search.

Sequences with E-value BETTER than threshold

Sequences producing significant alignments:

Score (bits)	E Value
909	0.0
303	2e-81
294	1e-78
279	4e-74
220	3e-56
210	2e-53
205	5e-52
203	3e-51
195	8e-49
189	5e-47
178	9e-44
176	4e-43
175	6e-43
164	2e-39
158	1e-37
152	5e-36
148	9e-35
115	9e-25
108	1e-22
100	4e-20
95	1e-18
94	3e-18
86	5e-16
83	6e-15
82	1e-14
81	2e-14
81	2e-14
78	1e-13
76	5e-13
76	5e-13
76	6e-13
75	2e-12
71	3e-11
69	6e-11
69	8e-11
68	2e-10
66	5e-10
64	3e-09
64	3e-09
60	4e-08
60	4e-08
59	1e-07
58	2e-07
52	9e-06
48	2e-04

sp 059923 SIR2_CANAL	REGULATORY PROTEIN SIR2 >gi 3005095 gb AAC...	909	0.0
sp P33294 SIR2_KLULA	REGULATORY PROTEIN SIR2 (SILENT INFORMATIO...	303	2e-81
sp P53685 HST1 YEAST	HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1...	294	1e-78
sp P06700 SIR2 YEAST	REGULATORY PROTEIN SIR2 (SILENT INFORMATIO...	279	4e-74
gb AAD40849_1 AF083106_1	(AF083106) sirtuin type 1 [Homo sapiens]	220	3e-56
emb CAB38511_2	(AL035637) putative regulatory protein sir2-lik...	210	2e-53
gi 3928792	(AF068758) SIR2 [Drosophila melanogaster]	205	5e-52
emb CAB58129_1	(AL121807) putative SIR2-like transcriptional r...	203	3e-51
emb CAA94364_1	(Z70310) predicted using Genefinder; Similarity...	195	8e-49
gb AAD40851_1 AF083108_1	(AF083108) sirtuin type 3 [Homo sapiens]	189	5e-47
gb AAD40850_1 AF083107_1	(AF083107) sirtuin type 2 [Homo sapiens]	178	9e-44
emb CAA22018_1	(AL033503) transcription regulatory protein [Cand...	176	4e-43
gb AAD45971_1 AF095714_1	(AF095714) silencing information regul...	175	6e-43
sp Q25337 SIR2 LEIMA	REGULATORY PROTEIN SIR2 HOMOLOG (LMSIR2RP)...	164	2e-39
sp P53686 HST2 YEAST	HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2...	158	1e-37
gb AAD20046_1	(AF131800) Similar to rat 5E5 antigen [Homo sapiens]	152	5e-36
gi 3860233	(AF102869) Sir2 homolog [Trypanosoma brucei]	148	9e-35
sp P53687 HST3 YEAST	HST3 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 3...	115	9e-25
gb AAD35575_1 AE001726_9	(AE001726) regulatory protein, SIR2 fa...	108	1e-22
gi 2650531	(AE001098) transcriptional regulatory protein, Sir2 ...	100	4e-20
emb CAA74510_1	(Y14082) hypothetical protein [Bacillus subtili...	95	1e-18
gb AAD53752_1 AF173939_1	(AF173939) Hst4p [Schizosaccharomyces ...	94	3e-18
gi 845686	(M32103) ORF-27 [Staphylococcus aureus]	86	5e-16
gi 2648874	(AE000987) transcriptional regulatory protein, Sir2 ...	83	6e-15
dbj BAA80785_1	(AP000062) 247aa long hypothetical protein [Aer...	82	1e-14
gi 2984374	(AE000776) hypothetical protein [Aquifex aeolicus]	81	2e-14
gb AAD40853_1 AF083110_1	(AF083110) sirtuin type 5 [Homo sapiens]	81	2e-14
emb CAB50112_1	(AJ248286) transcriptional regulatory protein, ...	78	1e-13
sp P53688 HST4 YEAST	HST4 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 4...	76	5e-13
gb AAD42226_1 AF159133_1	(AF159133) SIR2-like protein [Oryza sa...	76	5e-13
dbj BAA30044_1	(AP000004) 249aa long hypothetical protein [Pyroc...	76	6e-13
gb AAD15478_1	(AC006930) R33423_1 [Homo sapiens]	75	2e-12
emb CAB56682_1	(AL121596) putative SIR2-like regulatory protei...	71	3e-11
gb AAD40852_1 AF083109_1	(AF083109) sirtuin type 4 [Homo sapiens]	69	6e-11
gb AAC70895_1	(AF006830) unknown [Actinobacillus actinomycetemco...	69	8e-11
emb CAB09010_1	(Z95584) hypothetical protein Rv1151c [Mycobacter...	68	2e-10
emb CAA90546_1	(Z50177) similar to SIR; cDNA EST yk300f10.3 co...	66	5e-10
gb AAB95634_1	(AC003982) unknown function; 60% similar to Z50177...	64	3e-09
gi 4155790	(AE001545) putative [Helicobacter pylori J99]	64	3e-09
emb CAA90547_1	(Z50177) similar to SIR [Caenorhabditis elegans]	60	4e-08
gi 2996605	(U89687) putative nicotinic acid mononucleotide:5, 6...	60	4e-08
gi 1787364	(AE000212) putative nicotinic acid mononucleotide:5, 6...	59	1e-07
gi 1943780	(U97193) similar to S. cerevisiae SIR2 (SP:PO6700) a...	58	2e-07
emb CAA22773_1	(AL035206) putative SIR2 family transcriptional r...	52	9e-06
emb CAB55543_1	(AL117324) possible sirtuin [Leishmania major]	48	2e-04

Sequences with E-value WORSE than threshold

gb AAD08305_1	(AE000631) conserved hypothetical protein [Helic...	45	0.001
gi 3548790	(AC005620) R33590_2, partial CDS [Homo sapiens]	35	1.3
sp P44781 HEPA_HAEIN	RNA POLYMERASE ASSOCIATED PROTEIN HOMOLOG ...	34	2.2
emb CAB59689_1	(AL132675) zinc-finger protein [Schizosaccharom...	34	2.8
sp P32863 RA54 YEAST	DNA REPAIR AND RECOMBINATION PROTEIN RAD54...	33	6.3
emb CAA22741_1	(AL035205) putative SIR2 family transcriptional r...	33	6.3

Alignments

sp|059923|SIR2_CANAL REGULATORY PROTEIN SIR2 >gi|3005095|gb|AAC09304.1| (AF045774) SIR2
[Candida albicans]
Length = 515

Score = 909 bits (2323), Expect = 0.0
Identities = 451/515 (87%), Positives = 451/515 (87%)

Query: 1 MTTFWSQTINRQNXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXKGMITPTPXXXXXX 60
MTTFWSQTINRQN KGMITPTP
Sbjct: 1 MTTFWSQTINRQNQNGGVATATATAATATTPTAGGTGAGTTSTKGMITPTPFNIDINN 60

Query: 61 XXXXXXGKFIELTFKPDLELQQKYRSFIQREGALSFPRTETTQSMSKRDICALILNLGYPK 120
GKFIELTFKPDLELQQKYRSFIQREGALSFPRTETTQSMSKRDICALILNLGYPK
Sbjct: 61 DLNDFDGKFIETFKPDLELQQKYRSFIQREGALSFPRTETTQSMSKRDICALILNLGYPK 120

Query: 121 KAVEDYPIIILTKELAYILLKMLMTDSAQLEPKVEIDENDNKXXXXXXXXXXXXXX 180
KAVEDYPIIILTKELAYILLKMLMTDSAQLEPKVEIDENDNK
Sbjct: 121 KAVEDYPIIILTKELAYILLKMLMTDSAQLEPKVEIDENDNKNDGTNNSDIDSNSDMDSQS 180

Query: 181 ESGELGDAMDVDDSLPENEDEYDQDMSTTLKRTINMTPFKYKLPLDISLDRAKKIMVV 240
ESGELGDAMDVDDSLPENEDEYDQDMSTTLKRTINMTPFKYKLPLDISLDRAKKIMVV
Sbjct: 181 ESGELGDAMDVDDSLPENEDEYDQDMSTTLKRTINMTPFKYKLPLDISLDRAKKIMVV 240

Query: 241 TGAGISTSLGIPDPRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIAHVLPPDG 300
TGAGISTSLGIPDPRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIAHVLPPDG
Sbjct: 241 TGAGISTSLGIPDPRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIAHVLPPDG 300

Query: 301 KFSLLHAFLKLLQDKHKLLRNNTQNIDNLEQRAGLKSEKLVQCHGSFAKAKCVSCQGIFA 360
KFSLLHAFLKLLQDKHKLLRNNTQNIDNLEQRAGLKSEKLVQCHGSFAKAKCVSCQGIFA
Sbjct: 301 KFSLLHAFLKLLQDKHKLLRNNTQNIDNLEQRAGLKSEKLVQCHGSFAKAKCVSCQGIFA 360

Query: 361 GEKIYNHIRRQVPRCAICWKNTQAPIHFGAIKPITFFGEDLPERFHTLMDKDLQQID 420
GEKIYNHIRRQVPRCAICWKNTQAPIHFGAIKPITFFGEDLPERFHTLMDKDLQQID
Sbjct: 361 GEKIYNHIRRQVPRCAICWKNTQAPIHFGAIKPITFFGEDLPERFHTLMDKDLQQID 420

Query: 421 LFLVIGTSLKVEPVASIIERPVYKVPKILINKDPIPNRGFLNQLGLCDAVSYLCKCLK 480
LFLVIGTSLKVEPVASIIERPVYKVPKILINKDPIPNRGFLNQLGLCDAVSYLCKCLK
Sbjct: 421 LFLVIGTSLKVEPVASIIERPVYKVPKILINKDPIPNRGFLNQLGLCDAVSYLCKCLK 480

Query: 481 WDIPHADFNNDDELKLSKLKNGDWEIVNKSTSTKK 515
WDIPHADFNNDDELKLSKLKNGDWEIVNKSTSTKK
Sbjct: 481 WDIPHADFNNDDELKLSKLKNGDWEIVNKSTSTKK 515

sp|P33294|SIR2_KLULA REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2)
>gi|480276|pir||S36616 SIR2 protein - yeast
(Kluyveromyces marxianus var. lactis)
>gi|1362250|pir||A56048 regulatory protein SIR2 - yeast
(Kluyveromyces marxianus var. lactis)
>gi|397350|emb|CAA52661| (X74569) SIR2 [Kluyveromyces
lactis]
Length = 670

Score = 303 bits (769), Expect = 2e-81
Identities = 154/323 (47%), Positives = 205/323 (62%), Gaps = 34/323 (10%)

Query: 204 QDMSTTTLKRTINMTPFKYKLPLDISLDRAKKIMVVTGAGISTSLGIPDPRSFKGLYNQ 263
Q L I +T F + + D ++ L AKKI+V+TGAGISTSLGIPDPRSF +G Y++
Sbjct: 281 QKAMNKVLSTRIRLTFN- HTIDDFVAKLKTAKKIIVLTGAGISTSLGIPDPRSFSEGFY SK 339

Query: 264 LSKLNLSDPQKVFDLQTFMREGRLFYTIAHVLPPDGKFSLLHAFLKLLQDKHKLLRNNT 323
L L L+DPQ VF L+ F + +FY IAH+VLPP+ +S LH+F+K++QDK KLLRNNT
Sbjct: 340 LGDGLNLPQDVFSLEVFTEDPSVFYNIAMVLPPENMYSPLHSFIKMIQDKDKLRRNYT 399

Query: 324 QNIDNLEQRAGLKSEKLVQCHGSFAKAKCVSCQGIFAGEK IYNHIRRQVPRCAICWK-- 381
QNIDNLE AG++ EK+VQCHGSFA A CV+C GE+I+ +IR Q+P C C+
Sbjct: 400 QNIDNLESYAGVEPEKMVQCHGSFATASCVTCHWKIQGERIFPNIRNLQLPICPYCSKR 459

Query: 382 -----NTKQAPIHFGAIKPITFFGEDLPERFHTLMDKDLQQ 418
+ + P FG +KP ITFFGE LP +FH L+ +D+ Q
Sbjct: 460 LEFFKTKTDEELADGEDDDMDDHGRSRVPKSFGVLKPDITFFGEALPSKFHRLIREDVLIQ 519

Query: 419 IDLFLVIGTSLKVEPVASIIERPVYKVPKILINKDPIPNRGFLNQLGLCDAVSYLCKC 478
DL + IGTSLKV PV+ I+ +P VP+ +LINKDP+ + F+L LLGLCDD + + +
Sbjct: 520 CDLLICIGTSLKVAPVSEIVNMIPAHVPQVLINKDPVKHAEFDLSLLGLCDDVAALVAQK 579

Query: 479 LKWDIPHADFNNDDELKLSKLKN 501
WDIPH ++N KLN
Sbjct: 580 CGWDIPHHDNWNN-----KLN 594

sp|P53685|HST1_YEAST HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1) >gi|2120023|pir||S59698
HST1 protein - yeast (Saccharomyces cerevisiae)
>gi|972893 (L47120) homolog of SIR2; transcribed ORF
flanked by NUF2 (X72225) and RTG1 (M97690)
[Saccharomyces cerevisiae] >gi|1055020 (U39041) Hst1p
[Saccharomyces cerevisiae] >gi|1419891|emb|CAA99078|
(Z74810) ORF YOL068c [Saccharomyces cerevisiae]

Length = 503

Score = 294 bits (744), Expect = 1e-78
Identities = 144/275 (52%), Positives = 187/275 (67%), Gaps = 20/275 (7%)

Query: 231 LSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYT 290
L AKKI+V+TGAG+STSLGIPPDFRS +G Y+++ L L DPQ VF+L F+++ +FY
Sbjct: 197 LRNAKKILVLTGAGVSTSLGIPDFRSSEGFYSKIRHLGLEDPQDVFNLDIFLQDPSVFYN 256

Query: 291 IAHVLVPPDGKFSLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLKSEKLVQCHGSFAKA 350
IAH+VLPP+ +S LH+F+K+LQDK KLLRNYTQNIDNLE AG+ +KLVQCHGSFA A
Sbjct: 257 IAHMVLPPENMYSPLHSFIKMLQDKGKLLRNYTQNIDNLESYAGIDPDFKLVQCHGSFATA 316

Query: 351 KCVSCQGIFAGEKEIYNHIRRKQVPRCAICWKNTKQ-----API--HF 390
CV+C GEKI+ +IR ++P C C++ KQ +PI +
Sbjct: 317 SCVTCHWQ1PGEKIFENIRNLELPLCPYCYQKRKQYFPMSNGNNNTVQTININFNSPILKSY 376

Query: 391 GAIKPTITFFGEDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVKILI 450
G +KP +ITFGE LP RFH + KD+ + DL + IGTSLK V PV+ I+ VP VP+ILLI
Sbjct: 377 GVLKPDMTFFGEALPSRFHKTIRKDILECDLLICIGTSLKVAPVSEIVNMVPSHVPQILI 436

Query: 451 NKDPIPNRGFNLQLLGLCDAVSYLCCKLWDIPH 485
N+D + + F+L LLG CDD S + K WDIPH
Sbjct: 437 NRDMVTTHAEFDLNLLGFCDDVASLVAKKCHWDIPH 471

sp|P06700|SIR2_YEAST REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2)
>gi|73251|pir||RGByS2 regulatory protein SIR2 - yeast
(Saccharomyces cerevisiae) >gi|4470|emb|CAA25667|
(X01419) SIR2 protein [Saccharomyces cerevisiae]
>gi|1279674|emb|CAA96447| (Z71781) SIR2 [Saccharomyces cerevisiae]
>gi|1431027|emb|CAA98600| (Z74090) ORF
YDL042c [Saccharomyces cerevisiae]
Length = 562

Score = 279 bits (706), Expect = 4e-74
Identities = 140/314 (44%), Positives = 197/314 (62%), Gaps = 27/314 (8%)

Query: 222 YKLPDLISDSLRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTF 281
+ + I L A+K+V+TGAG+STSLGIPPDFRS +G Y+++ L L DPQ VF+ F
Sbjct: 242 FTIDHFIQKLHTARKILVLTGAGVSTSLGIPDFRSSEGFYSKIKHGLDPPQDVFNYNIF 301

Query: 282 MREGRLFYTI AHLVLPDGKFSLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLKSEKLV 341
M + +FY IA++VLPP+ +S LH+F+K+LQ K KLLRNYTQNIDNLE AG+ ++KLV
Sbjct: 302 MHDPGVFYNIANMVPPEKIYSPHSFIKMLQMKGKLLRNYTQNIDNLESYAGISTDKLV 361

Query: 342 QCHGSFAKAKCVSCQGIFAGEKEIYNHIRRKQVPRCAICWKNTKQ----- 385
QCHGSFA A CV+C GE+I+N IR ++P C C+K ++
Sbjct: 362 QCHGSFATATCVTCHWNLPGERIFNKIRNLELPLCPYCYKRRREYFPEGYNNKVGVAAQ 421

Query: 386 -----APIH----FGAIKPTITFFGEDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVAS 436
P + +G +KP ITFFGE LP +FH + +D+ + DL + IGTSLK V PV+
Sbjct: 422 GSMSERPPYILNSYGVLPKDITFFGEALPNKFHKSIREDILECDLLICIGTSLKVAPVSE 481

Query: 437 IIERPYPYKVKPILINKDPIPVRGNFLQLLGLCDAVSYLCCKLWDIPHADFNN--NDEL 494
I+ VP VP++LIN+DP+ + F+L LLG CDD + + + W IPH +N+ N
Sbjct: 482 IVNMVPSHVPQVLINRDPVKHAEFDLSSLGYCDDIAAMVAQKCGWTIPHKKWNDLKNKF 541

Query: 495 KLSKLKNGDWIEVN 508
K + G + + +
Sbjct: 542 KCQEKDKGVYVVT 555

gb|AAD40849.1|AF083106_1 (AF083106) sirtuin type 1 [Homo sapiens]
Length = 555

Score = 220 bits (554), Expect = 3e-56
Identities = 116/255 (45%), Positives = 164/255 (63%), Gaps = 9/255 (3%)

Query: 224 LPDLISDSLRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSK--LNLSDPQKVFDLQTF 281
+ D + L KKI+V+TGAG+S S GIPDFRS G+Y +L+ +L DPQ +FD++ F
Sbjct: 51 IEDAVKLLQECKKIIIVLTGAGVSVSCGIPDFRSRDGIYARLAVIDFPDLPDPQAMFDIEYF 110

Query: 282 MREGRLFYTI AHLVLPDGKFSLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLKSEKLV 341
++ R F+ A + P + SL H F+ L + KLLRNYTQNID LEQ AG+ +***
Sbjct: 111 RKDPRPFFKFAKEIYPGQFQPSLCHKFIALSDKEGKLLRNYTQNIDTLEQVAGI--QRII 168

Query: 342 QCHGSFAKAKCVSCQGIFAGEKEIYNHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFG 401
QCHGSFA A C+ C+ E+ I + VPRC C A +KP I FFG
Sbjct: 169 QCHGSFATASCLICKYKVDCEAVRGDIFNQVVPRCPRC----PADEPLAIMKPEIVFFG 223

Query: 402 EDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVKPILINKDPIPVRGN 461
E+LPE+FH M D ++DL +VIG+SLKV PVA I +P++VP+ILIN++P+P+ F+
Sbjct: 224 ENLPEQFHRAMKYDKDEVDILLIVIGSSLKVRPVALIPPSSIPHEVQPILINREPLPHLHFD 283

Query: 462 LQLLGLCDAVSYLC 476
++LLG CD ++ LC
Sbjct: 284 VELLGDCDVIINELC 298

emb|CAB38511.2| (AL035637) putative regulatory protein sir2-like
 [Schizosaccharomyces pombe]
 Length = 471

Score = 210 bits (530), Expect = 2e-53
 Identities = 122/325 (37%), Positives = 182/325 (55%), Gaps = 35/325 (10%)

Query: 189 MDVDDSLPENEDEYQDMSTTLKRTINMTPFKYKLP-----DLISDLRAKKIMVVVTG 242
 + + + + L E ED + + LKR + + KLP D+++ L +AK ++V+ G
 Sbjct: 104 INLPSALEEFEDIDLLPLLKVEVLKREVAR---RIKLPHFNTFEDVNVLKKA
 KAKNVVVLVG 160

Query: 243 AGISTSLGIPDFRSFKGGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTI AHLVLPPDGKF 302
 AGISTSLGI DFRS G Y +L++ LS+P ++FD+ TF +FYT A +LP +
 Sbjct: 161 AGISTSLGILDFRSNDNGFYARLARHGLSEPSEMDIHTFRENPEIFYTFARDLLPETNHY 220

Query: 303 SLLHAFLKLLQDKHKLRLNYTQNIDNLEQRAGLKSEKLVQCHGSFAKACVSCQGIFAGE 362
 S HAF++LL+ K+KL +TQNIDNLE++ GL K++QCHGSFA A C+ C+ G
 Sbjct: 221 SPSPHAFLRLEKKNNKLSTLFTQNI
 DNLEKKTGLSDNKIIQCHGSFATATCIKCKHKVDGS 280

Query: 363 KIYNHIRRKQVPRCAICWK-----NTKQAPIHF-----GAIKPTIT 398
 ++Y IR ++V C C K K+ +F G +KP IT
 Sbjct: 281 ELYEDIRNQRVSYCNECGKPPKLRLRVGQNKKEKHYFSDGDSESED
 DLAQPGIMKPDIT 340

Query: 399 FFGEDLPERFHTLMDK-DLQQIDLFLVIGTSKLKVEPVASIIERVPYKVKILINKDPIPN 457
 FFGE LP+ F + +L++ DL + IGTSLKV PV+ +I +P P+I I++ P+ +
 Sbjct: 341 FFGEALPDSSFNKVGSGELETDLICIGTSKLKVAPVSELISVIPPTTPQIYISRTPVRH 400

Query: 458 RGFNLQLLG-LCDDAVSYLCKCLKW 481
 F++ L CD + +CK W
 Sbjct: 401 TQFDVNFLSPYCDWVIVEICKRAGW 425

gi|3928792 (AF068758) SIR2 [Drosophila melanogaster]
 Length = 823

Score = 205 bits (517), Expect = 5e-52
 Identities = 111/269 (41%), Positives = 167/269 (61%), Gaps = 20/269 (7%)

Query: 226 DLISDLRAKKIMVVVTGAGISTSLGIPDFRSFKGGLYNQLSK--LNLSDPQKVFDLQTFMR 283
 D+IS + + +KI+V+TGAG+S S GIPDFRS G+Y +L+ +L DPQ +FD+ F R
 Sbjct: 211 DVISLVKKSQKIIIVLTGAGVS
 VSCGIPDFRSTNGYIARLAHD
 FPDLPDPQAMFDINYFKR 270

Query: 284 EGRLFYTIIAHLVLPPDGKF---SLLHAFLKLLQDKHKLRLNYTQNIDNLEQRAGLKSEKLV 341
 + R FY A + P + F S H F+K+L+ K KLLRN
 YTQNID LE+ AG+ + + +
 Sbjct: 271 DPRPFYKFAREIY
 PGEFQFQPS
 PCHRFI
 KMLETKGKLLRN
 YTQNIDTL
 ERVAGI--QRVI 328

Query: 342 QCHGSFAKACVSCQGIFAGEK
 IYHN
 HIRRKQVPRCAICWKNTKQAP----- 387
 +CHGSF+ A C C+ + + I + + +P C C N +Q+
 Sbjct: 329 ECHGSFSTASCTKCRFKCNADALRAD
 IFQA
 RIPVCPQCQPNKEQSVDASVA
 TEEELRQL 388

Query: 388 IHFGAIKPTITFFF
 GEDLPERFHTLMDKDLQQIDLFLVIGTSKLKVEPVASIIERVPYKVKP
 447
 + G +KP I FFGE LP+ +HT+M D DL +VIG+SLKV PVA I +P VP+
 Sbjct: 389 VENGIMKPDIVFF
 GEGLPDEYHTVMATDKDV
 C DLLIVIGSSLKVR
 PVAHIPSSIPATV
 PQ 448

Query: 448 ILINKDPIPNRGFNQLLGLCDDAVSYLC 476
 ILIN++ + + F+++LLG D ++ +C
 Sbjct: 449 ILINREQLHHLKFDVELLGDS
 DSVIINQIC 477

emb|CAB58129.1| (AL121807) putative SIR2-like transcriptional regulatory protein
 [Schizosaccharomyces pombe]
 Length = 332

Score = 203 bits (511), Expect = 3e-51
 Identities = 114/263 (43%), Positives = 156/263 (58%), Gaps = 15/263 (5%)

Query: 223 KLPDLISDLRAKKIMVVVTGAGISTSLGIPDFRSFK-GLYNQLSKLNLSDPQKVFDLQTF 281
 K+ LI + + KKI V+ GAGIST+ GIPDFRS + G+Y N L + NL + VFDL F
 Sbjct: 17 KV
 ASLIKE-GKV
 KKICV
 MVGAGISTAAGI
 PDRSPETGIY
 NNLRQFNL
 PYAEAVFDLSYF 75

Query: 282 MREGRLFYTIIAHLVLPPDGKFSLLHAFLKLLQDKHKLRLNYTQNIDNLEQRAGLKSEKLV 341
 + R FY +AH ++P + + H F++L L DK L + YTQNID LE+ AG+ + L+
 Sbjct: 76 RKNP
 PRPFYELA
 HLMPEKYR
 PTYTHYF
 IRLHD
 KRLLQ
 KCYTQNID
 TLERLAG
 VPDKALI 135

Query: 342 QCHGSFAKACVSCQGIFAGEK
 IYHN
 HIRRKQVPRCAICWKNTKQAP
 IHFGAIKPTITFFF 401
 + HGSF + +C+ C + E + I +KQVP+C C G IKP I F+G
 Sbjct: 136 EA
 HGSFQYSRCIECYEMA
 ETYE
 VRCACIM
 MQKQV
 PKCN
 SC-----KGLIKPMIVFYG 185

Query: 402 EDLPERFHTLMDKDLQQIDLFLVIGTSKLKVEPVASIIERVPYKVKILINKDP---IPNR 458
 E LP RF M+KD + D+ LVI
 GTSL V P A + E VP K + +LIN++P R
 Sbjct: 186 EGLPMRFFEH
 MEKDTK
 VCDMA
 LVI
 GH
 P
 FADL
 PEIV
 PN
 K
 QR
 VL
 LIN
 REPAGDFGER 245

Query: 459 GFNLQLLGLCDDAVSYLCKCLKW 481
 ++ +LG CD V LCK L W
 Sbjct: 246 KK
 DIMILG
 DCDSQ
 VR
 ALCK
 LLGW 268

emb|CAA94364.1| (Z70310) predicted using Genefinder; Similarity to K.lactis

regulatory protein SIR2 (SW:SIR2_KLULA); cDNA EST
EMBL:Z14446 comes from this gene; cDNA EST yk352g2.5
comes from this gene [Caenorhabditis elegans]
Length = 607

Score = 195 bits (490), Expect = 8e-49
Identities = 106/255 (41%), Positives = 147/255 (57%), Gaps = 14/255 (5%)

Query: 224 LPDLISDLSRAKKIMVVTGAGISTSLGIPPDFRSFKGLYNQLSKL--NLSDPQKVFDLQTF 281
L D + K I+V+TAGG+S S GIPDFRS G+Y +L +L DP +F++ F
Sbjct: 135 LADAVELFKTKKHLVLTGAGVSVSCGIGPDFRSKDGIYARLRSEFPDLPPTAMFDIYF 194

Query: 282 MREGRLFYTIAHVLVLPDGKFSLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLKSEKLV 341
FY A + P S+ H F+K L+ +LLRNYTQNID LE + G+K ++V
Sbjct: 195 RENPAPFVNFAREIFPGQFVPSVSHRFIKELETSGRLLRNYTQNIDTLEHQQTGIK--RVV 252

Query: 342 QCHGSFAKAKCVSCQGIFAGEKEIYHNHIRRQVPRCAICWKNTKQAPIHFGAIKPTITFFG 401
+CHGSF+K C C + G +I + +V C C G IKP I FFG
Sbjct: 253 ECHGSFSKCTCTRCGQKYDGNEIREEVLAMRVAHCKRCE-----GVIKPNIVFFG 302

Query: 402 EDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVPKILINKDPIPNRGFN 461
EDL FH + +D ++DL +VIG+SLKV PVA I V VP+ILIN++ +P+ +
Sbjct: 303 EDLGREFHQHVTEDKHVVDLIVVIGSSLKVRPVALIPHCVDKNVPQILINRESLPHYNAD 362

Query: 462 LQLGLCDDAVSYLC 476
++LLG CDD + +C
Sbjct: 363 IELLGNCDDIIRDIC 377

[gb|AAD40851.1|AF083108_1](#) (AF083108) sirtuin type 3 [Homo sapiens]
Length = 399

Score = 189 bits (475), Expect = 5e-47
Identities = 117/285 (41%), Positives = 162/285 (56%), Gaps = 21/285 (7%)

Query: 221 KYKLPDLISDLSRAK---KIMVVTGAGISTSLGIPPDFRS-FKGLYNQLSKLNLSDPQKV 276
K L D +++L RA+ ++V+ GAGIST GIPDFRS GLY+ L + +L P+ +F
Sbjct: 122 KLSLQD-VAEELIRARACQRVVVMVGAGISTPSGIPDFRSPEGSGLYSNLQQYDLPYPEAIF 180

Query: 277 DLQTFMREGRLFYTIAHVLVLPDGKFSLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLK 336
+L F + F+T+A + P + K ++ H FL+LL DK LLR YTQNID LE+ +G+
Sbjct: 181 ELPFFFHNPKPFFTLAKELYPGNYKPNVTHYFLRLLHDKGLLLRLYTQNIDGLERVSGIP 240

Query: 337 SEKLVQCHGSFAKAKCVSCQGIFAGEKEIYHNHIRRQVPRCAICWKNTKQAPIHFGAIKPT 396
+ KLV+ HG+FA A C CQ F GE I + +VPRC +C G +KP
Sbjct: 241 ASKLVEAHGTFASATCTVCQRPFPGEDIRADMADRVPVPCPVC-----TGVVKPD 290

Query: 397 ITFFGEDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVPKILINKDPI- 455
I FFGE LP+RF L D DL L+GTSL+VEP AS+ E V VP++LIN+D +
Sbjct: 291 IVFFGEPLPQRF-LLHVVDFFPMADLLLILGTSLEVEPFAASLTERAVRSSVPRLLINRDLVG 349

Query: 456 ----PNRGFNQLLGLCDDAVSYLCKCLKWDIPHADFNNDDELKL 496
R ++ LG V L + L W D + KL
Sbjct: 350 PLAWHPRSRDVAQLGDVVHGVESLVELLGWTEEMRDLVQRETGKL 394

[gb|AAD40850.1|AF083107_1](#) (AF083107) sirtuin type 2 [Homo sapiens]
Length = 373

Score = 178 bits (447), Expect = 9e-44
Identities = 101/264 (38%), Positives = 150/264 (56%), Gaps = 21/264 (7%)

Query: 201 EYDQDMSTTLKRTINMTPFKYKLPDLIS-----DLSRAKKIMVVTGAGISTSLGIP 252
E D D +T+++ K +L D ++ R +++++ + GAGISTS GIP
Sbjct: 19 EADMDFLRLNLSFSQLTSLGSQKERLLDELTLEGVARYMQSERCRRVICLVGAGISTSAGIP 78

Query: 253 DFRS-FKGLYNQLSKLNLSDPQKVFDLQTMREGRLFYTIAHVLVLPDGKFSLLHAFLKL 311
DFRS GLY+ L K +L P+ +F++ F+ F+ +A + P K ++ H F++L
Sbjct: 79 DFRSPSTGLYDNLEKYHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRL 138

Query: 312 LQDKHKLLRNYTQNIDNLEQRAGLKSEKLVQCHGSFAKAKCV--SCQGIFAGEKEIYHNIR 369
L+DK LLR YTQNID LE+ AGL+ E LV+ HG+F + CV SC+ + + I
Sbjct: 139 LDKGLLLRCYTNQIDTLERIAGLEQEDLVEAHGTFYTSCHVASCRCHEYPLSWMKEKIF 198

Query: 370 RKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTLMDKDLQQIDLFLVIGTSL 429
+ P+C C +KP I FFGE LP RF + M D ++DL LV+GTSL
Sbjct: 199 SEVTPKCEDCQ-----SLVKPDIVFFGESLPPARFFSCMQSDFLKV DLLVMGTSL 248

Query: 430 KVEPVASIIERVPYKVPKILINKD 453
+V+P AS+I + P P++LINK+
Sbjct: 249 QVQPFASLISKAPLSTPRLLINKE 272

[emb|CAA22018_1](#) (AL033503) transcription regulatory protein [Candida albicans]
Length = 331

Score = 176 bits (441), Expect = 4e-43
Identities = 106/285 (37%), Positives = 154/285 (53%), Gaps = 20/285 (7%)

Query: 224 LPDLISDLSRA---KKIMVVTGAGISTSLGIPDFRS-FKGLYNQLSKLNLSDPQKVFDL 278
L D++ ++ A KK+ GAGIST GIPDFRS GLY L+KLN + VFD+
Sbjct: 4 LDDILKPVAEAVKNGKKVTFNGAGISTGAGIPDFRSPDTGLYANLAKLNLPFAEAVFDI 63

Query: 279 QTFMREGRLFYTIAHLVLPPDGKFSLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSE 338
F + + FYT+A + P + + H F+KLLQD+ L R YTQNID LE+ AG++ +
Sbjct: 64 DFFKEDPKPFYTLAEELYPGNFAPTKFHFIKLQDQGSLKRVYTQNIIDTLERLAGVEDK 123

Query: 339 KLVQCHGSFAKAKCVSCQGIFAGEKEIYNHIRRQVPRCAICWKNTKQAPIHFGAIKPTIT 398
+V+ HGSFA CV C E + +++ K++P C C G +KP I
Sbjct: 124 YIVEAHGSFASNHCVDCHKEMTTETLKTYMKDKKIPSCQHC-----EGYVKPDIV 173

Query: 399 FFGEGLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVPKILINKDPIPN- 457
FFGE LP +F L + D + +++ +V GTSL V P AS+ V K ++L+NK+ +
Sbjct: 174 FFGEGLPVKFSDLWEDDCEDVEAVAGTSLTVFFFASLPGEVNKKCLRVLVNKEKGTF 233

Query: 458 ---RGFNLLQGLCDDAVSYLCKCLKWDIPHADFNNNDEKLKSLK 498
R ++ L CD LC L D + +++K SK
Sbjct: 234 KHEPRKSIDIALLHCDIVAEKLCTLLGLDDKLNEVYEKEKIKYSK 278

gb|AAD45971.1|AF095714_1 (AF095714) silencing information regulator 2-like protein [Homo sapiens]
Length = 352

Score = 175 bits (440), Expect = 6e-43
Identities = 94/224 (41%), Positives = 136/224 (59%), Gaps = 13/224 (5%)

Query: 233 RAKKIMVVTGAGISTSLGIPDFRS-FKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIAH 291
R +++++ + GAGISTS GIPDFRS GLY+ L K +L P+ +F++ F + F+ +
Sbjct: 38 RCRRVICLVGAGISTSAGIPDFRSPSTGLYDNLEYHLPYPEAIFEISYFKHPEPFFAL 97

Query: 292 AHLVLPPDGKFSLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSEKLVQCHGSFAKAK 351
A + P K ++ H F++L+DK LLR YTQNID LE+ AGL+ E LV+ HQ+F +
Sbjct: 98 AKELYPGQFKPTICHYFMRLLKDKGLLLRCYTQNIIDTLERIAGLEQEDLVEAHGTFYTSH 157

Query: 352 CV--SCQGIFAGEKEIYNHIRRQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFH 409
CV SC+ + + I + P+C C +KP I FFGE LP RF
Sbjct: 158 CVSASCRCHEYPLSWMKEKIFSEVTPKCEDCQ-----SLVKPDIVFFGESLPARFF 207

Query: 410 TLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVPKILINKD 453
+ M D ++DL LV+GTSL+V+P AS+I + P P++LINK+
Sbjct: 208 SCMOSDFLKVDLLVMGTSIQLQPFASLISKAPLSTPRLLINKE 251

sp|Q25337|SIR2_LEIMA REGULATORY PROTEIN SIR2 HOMOLOG (LMSIR2RP) >gi|2133375|pir||JC4639
silent information regulator 2-related protein -
Leishmania major >gi|1203987 (L40331) homologous to
yeast silent information regulatory 2 protein
[Leishmania major]
Length = 381

Score = 164 bits (410), Expect = 2e-39
Identities = 95/245 (38%), Positives = 139/245 (55%), Gaps = 16/245 (6%)

Query: 235 KKIMVVTGAGISTSLGIPDFRSFK-GLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIAH 293
++I+V+ GAG S + GIPDFRS G+Y +L K NL DP F L + +FY+IA
Sbjct: 32 RRILVLVGAGASVAAGIPDFRSSDTGIYAKLGKYNLDDPTDAFSLTLLREKPEIFYSIAR 91

Query: 294 LVLPPDGKF-SLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSEKLVQCHGSFAKAK 351
+ G F + +H F++L+DK +LLR TQNID LE+ AG+ E LV+ HGSFA A
Sbjct: 92 ELNLWPQGHFQPTAVHHFIRLLQDEGRLLRCQTQNIIDGLEKAAGVSPELLVEAHGSFAAAA 151

Query: 352 CVSCQGIFAGEKEIYNHIRRQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFH 411
C+ C F+ E+ Y V RC+ C G +KP + FFGE+LP+ F
Sbjct: 152 CIECHTPFSIEQNYLEAMSGTVSRCSTCG-----GIVKPNVVFFGENLPDAFFDA 201

Query: 412 MDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVPKILINKDPIPBNRGFNL---QLLGLC 468
+ D +L ++IGTS++V P A + VP +P++L+N++ + F L +
Sbjct: 202 LHHDAPIAELVIIIGTSMQVHPFALLPCVVPKSIPRVLMNRRERVGGLLFRFPDDPLDTIH 261

Query: 469 DDAVS 473
DDAV+
Sbjct: 262 DDAVA 266

sp|P53686|HST2_YEAST HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2) >gi|2131291|pir||S59678
HST2 protein - yeast (Saccharomyces cerevisiae)
>gi|965078 (U33335) Lpa2p [Saccharomyces cerevisiae]
>gi|1055024 (U39063) Hst2p [Saccharomyces cerevisiae]
Length = 357

Score = 158 bits (395), Expect = 1e-37
Identities = 91/237 (38%), Positives = 131/237 (54%), Gaps = 27/237 (11%)

Query: 236 KIMVVTGAGISTSLGIPDFRS-FKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIAH 294
K++ + GAGISTS GIPDFRS GLY+ L++L L P+ VFD+ F + FYT+A
Sbjct: 26 KVIFMVGAGISTSCGIPDFRSPGTGLYHNLRALKLPYPEAVFDVDFQSDPLPFYTLAKE 85

Query: 295 VLPPDGKFSLLHAFLKLLQDKHKLRLNYTQNIDNLEQRAGLKSEKLVQCHGSFAAKCVS 354
 + P + S H LKL QDK L R YTQNID LE++AG+K + +++ HGSFA C+
 Sbjct: 86 LYPGNFRPSKFHYLLKLFQDKDVLKRVTQNIDTLERQAGVKDDLIEAHGSFAHCHCIG 145

 Query: 355 CGGIFAGEKEIYHIRR---KQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTL 411
 C ++ + + K +C + + + +KP I FFGEDLP+ F
 Sbjct: 146 CGKVYPPQVFQSKLAEHPIKDFVKCDVCGE-----LVKPAIVFFGEDLPDSFSET 195

 Query: 412 MDKDLQ-----QIDLFLVIGTSLKVEPVASIIERVPYKVPKILINKDPI 455
 D + Q L +V+GTSL V P AS+ E +P KV ++L N + +
 Sbjct: 196 WLNDSEWLREKITSGKHPQQPLVIVVGTSLAVYPFASLPEEIPRKVKRVLNCNLETV 252

[gb|AAD20046|](#) (AF131800) Similar to rat 5E5 antigen [Homo sapiens]
Length = 254

Score = 152 bits (381), Expect = 5e-36
Identities = 90/241 (37%), Positives = 133/241 (54%), Gaps = 21/241 (8%)

Query: 201 EYDQDMSTTLKRTINMTPFKYKLPDLIS-----DLSRAKKIMVVTGAGISTSLGIP 252
 E D D +T+++ K +L D ++ R +++++ + GAGISTS GIP
 Sbjct: 18 EADMDFLRLNLSQTLQLGSQKERLLDETLLEGVARYMQSERCRRVICLVGAGISTSAGIP 77

 Query: 253 DFRS-FKGLYNQLSKLNLSDPQKVFDLQTFMREGRRLFYTI AHLVLPPDGKFSLLHAFLKL 311
 DFRS GLY+ L K +L P+ +F++ F + F+ +A + P K ++ H F++L
 Sbjct: 78 DFRSPSTGLYDNLEKYHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRL 137

 Query: 312 LQDKHKLRLNYTQNIDNLEQRAGLKSEKLVQCHGSFAAKCV--SCQGIFAGEKEIYHIRR 369
 L+DK LLR YTQNID LE+ AGL+ E LV+ HG+F + CV SC+ + + I
 Sbjct: 138 LDKGULLRCYTQNIDTLERIAGLEQEDLVVAHGTFYTSCHVSASCRHEYPLSWMKEKIF 197

 Query: 370 RKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTLMDKDLQQIDLFLVIGTLS 429
 + P+C C +KP I FFGE LP RF + M D ++DL LV+GTSL
 Sbjct: 198 SEVTPKCEDCQ-----SLVKPDIVFFGESLPARFFSCMOSFLKVVDLLVMGTSL 247

 Query: 430 K 430
 +
 Sbjct: 248 Q 248

[gi|3860233|](#) (AF102869) Sir2 homolog [Trypanosoma brucei]
Length = 351

Score = 148 bits (370), Expect = 9e-35
Identities = 88/228 (38%), Positives = 124/228 (53%), Gaps = 14/228 (6%)

Query: 236 KIMVVTGAGISTSLGIPDFRS-FKGLYNQLSKLNLSDPQKVFDLQTFMREGRRLFYTI AHL 294
 KI V+ GAGIS + GIPDFRS GLY+ LS+ NL+ P+ F L ++ +FY I
 Sbjct: 31 KIFVMVGAGISVAAGIPDFRSPTGLYAKLSRYNLNNSPEDAFSLSPLLRQQPSVFNILMD 90

 Query: 295 VLPPDGKF--SLLHAFLKLLQDKHKLRLNYTQNIDNLEQRAGLKSEKLVQCHGSFAAKAC 352
 + GK+ + H F+ LL K LL TQNID LE+ G+ LV+ HGSF+ A C
 Sbjct: 91 MDLWPGKYCPPTTVHHFISLLAKGMLLCCCTQNIDGLERACGIPESLLVAHGSFSSASC 150

 Query: 353 VSCQGIFAGEKEIYHIRRQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTL 412
 V C + R +VP C C G +KP + FFGE+LPE F +
 Sbjct: 151 VDCHAKYDINIARAETRAGKVPHCNQCG-----GIVKPDVVFFGENLPEAFFNV 200

 Query: 413 DKDLQQIDLFLVIGTLSKVEPVASIIERVPYKVPKILINKDPIPNRGF 460
 ++ +L L++GTSL+V P A + VP VP++L N + + R F
 Sbjct: 201 GL-IEETELLILGTSLQVHPFADLALMVPSDVPRVLFNLERVGGRMF 247

[sp|P53687|HST3_YEAST](#) HST3 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 3) >gi|1078372|pir||S54631
HST3 protein - yeast (Saccharomyces cerevisiae)
>gi|829135|emb|CAA60741| (X87331) encodes homologue of
yeast SIR2 (controlling mating type); overlaps with
X01419 [Saccharomyces cerevisiae] >gi|1055022 (U39062)
Hst3p [Saccharomyces cerevisiae]
>gi|1420135|emb|CAA99215| (Z74933) ORF YOR025w
[Saccharomyces cerevisiae]
Length = 447

Score = 115 bits (285), Expect = 9e-25
Identities = 98/348 (28%), Positives = 161/348 (46%), Gaps = 63/348 (18%)

Query: 206 MSTTTLKRTINMTPFKYKLPDLISDLRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLS 265
 + T L I + L + LSR++I +TGAGIS + GIPDFRS GLY+ +
 Sbjct: 24 LQTEKLAHIIGLDADDEVLRVRTKQLSRSRRIACLTGAGISCNAGIPDFRSSDGLYDLVK 83

 Query: 266 K----LNLSDPQKVFDLQTFMREGRL-----FYTI AHLVLPPDGKFSLLHAFLKL 311
 K ++ +++FD+ F + ++ Y+ L P + H F+
 Sbjct: 84 KDCSQYWSIKSGREMFDISLFRDDFKISIFAKFMERLYSNVQLAKP----TKTHKFIAH 138

 Query: 312 LQDKHKLRLNYTQNIDNLEQRAGL-----KSEKLVQCHGSFAAKCVSC 355
 L+D++KLLR YTQNID LE+ GL K+ +VQ HG C C
 Sbjct: 139 LKDRNKLLRCYTQNIDGLEEISIGLTLNRKPLTSFSSHWKNLDVQLHGDLKTLSCTKC 198

 Query: 356 OGIFAGEKEIYNH-IRRQVPRCAICW-----KNTKQAPIHFGAIKPTITFFGEDLPE 406

F + ++ +RR ++P C C + + + G ++P I +GE+ P
Sbjct: 199 FQTFPWRSRYSRCLRRGELPLCPDEALINKRLNEGKRTLGSNVILRPNIVLYGENHPS 258

Query: 407 RFHTLMDKDLQQI---DLFLVIGTSLKVEPVASIIERVPYKVPK----ILINKDPIPNN 457
+L I D +++GTSLKVV+ V +++++ K+ IL+NK PI
Sbjct: 259 CEIITQGLNLDDIKGNPFDLIIIMGTSLKVDGVKQLVKKLSKKIHDRGGGLIILVNKTPIGE 318

Query: 458 RGF---NLQLLGLCDDAVSYLCKCLKWDIPHADFNNNDEL-KLSKLK 500
+ + Q+ CD+ V++ L+ IP F D++ KL +LK
Sbjct: 319 SSWHGIIDYQIHSDCDNWVTF---LESQIPDF-FKTQDQIKKLRLQQLK 361

gb|AAD35575.1|AE001726_9 (AE001726) regulatory protein, SIR2 family [Thermotoga maritima]
Length = 246

Score = 108 bits (267), Expect = 1e-22
Identities = 72/217 (33%), Positives = 106/217 (48%), Gaps = 21/217 (9%)

Query: 223 KLPDLISDLSSRAKKIMVVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFM 282
K+ + + L+ ++ + +TGAGIST GIPDFR G+Y + S Q VFD+ F
Sbjct: 2 KMKEFLDLLNESRLLTGTAGISTPSGIPDFRGPNNGIYKKYS-----QNVDIDFFY 54

Query: 283 REGRLFYTTIAHLVLPP--DGKFSLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSEKL 340
FY A + P K +L H L L++K + TQNIID L QRAG S+K+
Sbjct: 55 SHPEEFYRFAKEGIFPMLQAKPNLAHVLLAKLEEKGLIEAVITQNIIDRLHQAG--SKKV 112

Query: 341 VQCHGSFAKAKCVSCQGIFAGEKIYHNHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFF 400
++ HG+ + CV C+ + E + + VP C C I+P I FF
Sbjct: 113 IELHGNVEEYYCVRCEKKYTVEDVIKLESSDVPLCDC-----NSLIRPNIVFF 162

Query: 401 GEDLPERFHTEMDKDLQQIDLFLVIGTSLKVEPVASI 437
GE+LP+ + L +V+G+SL V P A +
Sbjct: 163 GENLPQDALREAIGLSSRASLMIVLGSSLVVYPAAEL 199

gi|2650531 (AE001098) transcriptional regulatory protein, Sir2 family
[Archaeoglobus fulgidus]
Length = 253

Score = 99.8 bits (245), Expect = 4e-20
Identities = 74/261 (28%), Positives = 124/261 (47%), Gaps = 36/261 (13%)

Query: 231 LSRAKKIMVVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFY 290
L+++K +V TGAGIS GIP FR GL+ + DP++V + F R R F+
Sbjct: 12 LAKSKHAVVFTGAGISAESGIPTRGEDGLWRKY-----DPEEVASISGFKRNPRAFW 65

Query: 291 IA----HLVLPDGFSLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSEKLVQCHG 345
+ L P+ H + L+ + TQNIID L QRAG S +++++ HG
Sbjct: 66 FSMEMKDNLFAEPNPA---HYAIAELERMGIVKAVITQNIIDMLHQAG--SRRVLELHG 119

Query: 346 SFAKAKCVSCQGIFAGEKIYHNHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLP 405
S K C+ C + + + ++PRC C +KP + FGE LP
Sbjct: 120 SMDKLDCLDCHETYDWSEFVDEFNKGEIPCRKCGSYY-----VKPRVVLFGEPLP 170

Query: 406 ERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIEVPYKVPK----ILINKDP-IPNRG 459
+R + + + D F+V+G+SL V P A + PY K I++N +P + +
Sbjct: 171 QRTLFEAIEEAKHCDAFMVVGSSLVVYPAAEL---PYIakkAGAKMIVNAEPTMADPI 226

Query: 460 FNLLQLLGLCDDAVSYLCKCLK 480
F+++++G + + + + +K
Sbjct: 227 FDVKIIGKAGEVLPKIVEEVK 247

emb|CAA74510.1| (Y14082) hypothetical protein [Bacillus subtilis]
>gi|2633300|emb|CAB12804| (Z99109) similar to
hypothetical proteins [Bacillus subtilis]
Length = 247

Score = 95.2 bits (233), Expect = 1e-18
Identities = 75/232 (32%), Positives = 114/232 (48%), Gaps = 22/232 (9%)

Query: 229 SDLSRAKKIMVVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLF 288
S L A++I+V+TGAG+ST GIPDFRS G++ + + L F+ RLF
Sbjct: 6 SILHEAQRIVVLTGAGMSTESGIPDFRSAGGIWTE-----DASRMEAMSLDYFLSYPRLF 60

Query: 289 Y----TIAHLVLPPDGKFSLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSEKLVQCH 344
+ + + + + + H L L+ + K + +TQNIID L ++AG S + + H
Sbjct: 61 WPKFKEFQMKMMSGSFEPNEGHLLAELKEQGKQVDIFTQNIIDGLHKKAG--SRHVYELH 118

Query: 345 GSFAKAKCVSCQGIFAGEKIYHNHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDL 404
GS A C +C + H+ ++VP C N I +K + FG D
Sbjct: 119 GSIQTAACPACGARYD---LPHLLEREVPECTAAGNN---GDICGTVLKTDVVLFG-DA 170

Query: 405 PERFHTEMDKDLQQIDLFLVIGTSLKVEPVASIIEVPY--KVPKILINKDP 454
F TL +K L Q DL LVIGTSL+V P + E + K++IN +P
Sbjct: 171 VMHFDTLYEK-LDQADLLLVIIGTSLEVAPARFVPEDASLIPGMKKVIINLEP 221

gb|AAD53752.1|AF173939_1 (AF173939) Hst4p [Schizosaccharomyces pombe]

Length = 415

Score = 93.6 bits (229), Expect = 3e-18
Identities = 99/330 (30%), Positives = 151/330 (45%), Gaps = 46/330 (13%)

Query: 224 LPDLISDLRSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLS---KLNLSDPQKVFDLQT 280
L L+S + +AK+I+VVTGAGIS GIPDFRS +GL++ L KLN S +++FD
Sbjct: 47 LSPLVSAIRKAKRIVVVVTGAGISCDAGIPDFRSSEGLFSSLRAEYKLNCSG-KELFDGSV 105

Query: 281 F--MREGRLFYTI AHL--VLPPDGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQR-AGL 335
+ ++ +F+ + +L + ++ H FL L + KLLR YTQNID LE R GL
Sbjct: 106 YRDLKSVNIFHAMIRKLHMLSNARPTDFHFLSQLAQEKSLLRLYTQNIDFLETLEG 165

Query: 336 KS-----EKLVQCHGSFAKAKCVSCQGIFAGEKIYHNIRRQVPRCAICWKNTK- 384
++ + + HG+ C C F + + R V C C +
Sbjct: 166 QTCIPLPQSAPWPPTIPLHGTLVEVSCTRS--FLKKFNPDIFDRNGVTCPDCKTENEV 223

Query: 385 -----QAPIHFGAIKPTITFGEDLP--ERFHLMKDLO-QIDLFLVIGTSLKVEPVAS 436
+ + G ++P I + E P E ++ +DL+ + D +V GTS K+ V
Sbjct: 224 RRIAGKRSVIEGCLRPRIVLYNEIHDPDSEISGVCSQDLKSRPCLIVAGTSCKIPGVKR 283

Query: 437 IIERVPYKVPK-----ILINKDPIP NRGFNLQQLLCDDA---SYLKCLK--WDIPH 485
II+ + V K I +N D P + F L LCD V + LK D P
Sbjct: 284 IIKEMNSNCVKQKG NVIWLNYDE-PTKDF---LNLCDLVVQGDLQIAIRRLKPLLDAPS 338

Query: 486 ADFNNNDELKLSKLKNGDWEIVNKSTSTKK 515
++ + SK K+ + + ST K
Sbjct: 339 WKLKSHSAKRTSKQKSSEQTKITSSTKITK 368

[gi|845686](#) (M32103) ORF-27 [Staphylococcus aureus]
Length = 243

Score = 86.2 bits (210), Expect = 5e-16
Identities = 68/238 (28%), Positives = 112/238 (46%), Gaps = 21/238 (8%)

Query: 221 KYKLPDLISDLRSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQT 280
K+ L L + + +I TGAG+S + G+PDFRS GL+ + +SK LS P+ +
Sbjct: 2 KHDLETLKHIIDSSNRITFFTGAGVSASGVPDFRSMGGLFDEISKDGLS-PEYLLSRDY 60

Query: 281 FMREGRLFYTI AHL--VLPPDGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQRAGLKSEK 339
+ F H +L D ++H ++ L+ + L TQNID L AG S+
Sbjct: 61 LEDDPEGFINFCHKRLLFVDTPNIVHDWIAKLERNQQSLGVITQNIDGLHSDAG--SQH 118

Query: 340 LVQCHGSFAKAKCVSCQGIFAGEKEIYHNIRRQVPRCAICWKNTKQAPIHFGAIKPTITF 399
+ + HG+ + C C + + + + C C GAI+P I
Sbjct: 119 VDELHGTLNRFYCNCVCHKSYTKSDVID---RTLKHDNCG-----GAIRPDIVL 164

Query: 400 FGEDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVPK-ILINKDPIP 456
+GE L + ++ D +V+G+SL V+P A +I +K I+INKD P
Sbjct: 165 YGEMLDQPTIIRALNKIEHADTLVVLGSSLVQPAAGLISH--FKGDNLIIINKDRTP 220

[gi|2648874](#) (AE000987) transcriptional regulatory protein, Sir2 family
[Archaeoglobus fulgidus]
Length = 245

Score = 82.7 bits (201), Expect = 6e-15
Identities = 65/238 (27%), Positives = 112/238 (46%), Gaps = 34/238 (14%)

Query: 227 LISDLRSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLS-----DPQKVFDLQ 279
L+ ++ +K ++ +TGAG+S GIP FR GL+N+ L+ DP+KV+
Sbjct: 5 LLKTIAESKYLVALTGAGVSAESGIFTFRGKDGLWNRYRPEELANPQAFAKDPEKVWKWY 64

Query: 280 TFMREGRLFYTI AHLVLPPDGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQRAGLKSEK 339
+ E ++F + + + H L+ L TQN+D+L +RAG S
Sbjct: 65 AWRME-KVF-----NAQPNKAHQAFELERLGLVKCLITQNVDDLHERAG--SRN 111

Query: 340 LVQCHGSFAKAKCVSCQGIFAGEKEIYHNIRRQVPRCAICWKNTKQAPIHFGAIKPTITF 399
++ HGS +C SC F ++ + +P+C C ++P + +
Sbjct: 112 VIHLHGSLLRVRCCTCNNSF---EVESAPKIPPLPKCDKCGS-----LLRPGVWW 158

Query: 400 FGEDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVPKIL-INKDPIP 456
FGE LP +++++ D+ +V GTS V+P AS+ V + I+ IN D P
Sbjct: 159 FGEMLPPDVLDRA MREVERADVIIVAGTSAVVQPAASLPLIVKQRGGAIEINPDETP 216

[dbj|BAA80785.1](#) (AP000062) 247aa long hypothetical protein [Aeropyrum pernix]
Length = 247

Score = 81.9 bits (199), Expect = 1e-14
Identities = 67/234 (28%), Positives = 107/234 (45%), Gaps = 33/234 (14%)

Query: 231 LSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLF-- 288
L+ ++ + TGAGIS GIP FR GL+++ +L+ P + F R+ RL
Sbjct: 13 LANSRFAVFTGAGISAESGIFTFRGKDGLWSRFDPRLATP-----EAFNRDPLVWE 66

Query: 289 ---YTI AHLVLPPDGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQRAGLKSEKLVQCHG 345
+ I ++ K H L L+D L TQN+D L +RAG S +++++ HG

Subjct: 67 WYSWRIERVLAAPKNK---AHRLRARLEDGVLKAVITQNVGLHRRAG--SRRVLELHG 121

Query: 346 SFAKAKCVSCQGIFAGEKI-YNHIRRQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDL 404
+ +A+C C G K+ + P C C G ++P + +FGE L
Sbjct: 122 NVLRARCTRC----GSKLEWRKEPSNLPPSCPRCG-----GVLRPDVVWFGEPL 166

Query: 405 PERFHILMDKDLQQIDLFLVIGTSLKVEPVASIIEERVPYKVPKILINKDPIPNR 458
++ D+ ++IGTS V+P A ++ + LIN +P PNR
Sbjct: 167 DTSLLLEAFGLARRSDVMIIIGTSGAVDP-AGLLPLAAKESGATLINVNPEPNR 219

gi|2984374 (AE000776) hypothetical protein [Aequifex aeolicus]
Length = 239

Score = 80.8 bits (196), Expect = 2e-14
Identities = 61/210 (29%), Positives = 98/210 (46%), Gaps = 37/210 (17%)

Query: 237 IMVVTGAGISTSLGIPPDFRSFKGLYNQLSKLNLSDPQKVFDLQTMREGRLFY----- 289
I+ +TGAGIS GIP FR GL+N+ L+ P + F R +L +
Sbjct: 6 IVTLTGAGISAESGIPTFRGKDGLWNKFKEELATP-----EAFFRNPKLVWEYWWDKR 59

Query: 290 TIAHLVLPPDGKFSLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSEKLVQCHGSFAK 349
+ P +G H L +++++ TQN+D L QRAG S+K+++ HG+ K
Sbjct: 60 QLIAKAQPNEG----HKILTKMEEFPNFTYLITQNVGDGLHQGRAG--SKVIELHGNIWK 112

Query: 350 AKCVSCQGIFAGEKEIYNNHIR--RKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPER 407
+CV C G + Y + + P+C C G ++P + +FGE LP
Sbjct: 113 VRCVEC----GNERYEYTTPLPEIPPCKECKG-----GLLRPGVVWFGEESLPVD 157

Query: 408 FHTLMDKDLQQIDLFLVIGTSLKVEPVASI 437
+ + ++ +F+V+GTS V P A +
Sbjct: 158 ALGRAYELSREAHVFIVVGTSGVVYPAAEL 187

gb|AAD40853.1|AF083110_1 (AF083110) sirtuin type 5 [Homo sapiens]
Length = 310

Score = 80.8 bits (196), Expect = 2e-14
Identities = 72/278 (25%), Positives = 120/278 (42%), Gaps = 37/278 (13%)

Query: 224 LPDLISDLSRAKKIMVVTGAGISTSLGIPPDFRSFKGLYNQLSKLNLS-----DPQKVF 276
+ D + +AK I+ +GAG+S G+P FR G + + +L+ +P +V+
Sbjct: 40 MADFRKFFAKAHKIVIISGAGVSAESGVPTFRGAGGYWRKWAQDLATPLAFAHNPSRVW 99

Query: 277 DLQTFMREGRLFYTI AHLVLPPDGKFSLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLK 336
+ + RE + P G ++ +L + +++++ TQNID L ++AG K
Sbjct: 100 EFYHYRRE-----VMGSKEPNAGHRAIAECETRLGKQGRVVV-ITQNIDELHRKAGTK 152

Query: 337 SEKLVQCHGSFAKAKCVSCQGIFAGEK--IYNHIRRQVPRCAICWKNTKQAPIHFG----- 390
+ L++ HGS K +C SC + K I + K P T+ A I
Sbjct: 153 N--LLEIHGSLKTRCTSGVVAENYKSPICPALSGKGPAPE----PGTQDASIPVEKLP 205

Query: 391 -----GAIKPTITFFGEDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIEERVP 442
G ++P + +FGE+L +D++L DL LV+GTS V P A +V
Sbjct: 206 RCEEAGCGLLLRPHVVWFGENLDPAILEEVDRLEAHCDLCLVVGTSSVVYPAAMFAPQVA 265

Query: 443 YK-VPKILINKDPIP-NRGFNLLQLLGLCDDAVSYLCKC 478
+ VP N + P F G C + C
Sbjct: 266 ARGVPVAEFNTEETTPATNRFRHFQGPCGTTLPEALAC 303

emb|CAB50112.1| (AJ248286) transcriptional regulatory protein, Sir2 family
[Pyrococcus abyssi]
Length = 250

Score = 78.4 bits (190), Expect = 1e-13
Identities = 59/211 (27%), Positives = 95/211 (44%), Gaps = 22/211 (10%)

Query: 231 LSRAKKIMVVTGAGISTSLGIPPDFRSFKGLYNQLSKLNLSDPQKVFDLQTMREGRLFY 290
L+ +K + TGAGIS G+P FR GL+N+ L+ P + F R +L +
Sbjct: 9 LASSKNAIAFTGAGISAESGVPTFRGKDGLWNKYRPEELATP-----EAFFRNPKLVWE 62

Query: 291 IAHLVLPP--DGKFSLLHAFLKLLQDKHKLLRNNTQNIIDNLEQRAGLKSEKLVQCHGSFA 348
+ K + H L L+D L TQN+D+L + AG ++ L++ HG+
Sbjct: 63 FYKWRINKILAKPNPAHYALVELEDMGILRAVITQNVDDLHREAGTRN--LIELHGNIF 120

Query: 349 KAKCVSC--QGIFAGEKEIYNNHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPE 406
+ KC C + + + ++ +P+C C ++P + +FGE LP
Sbjct: 121 RVKCTKCNFKKEYLKESQRLEEVLKEDLPCPRCG-----SLLRPDVVWFGEPLPR 170

Query: 407 RFHTLMDKDLQQIDLFLVIGTSLKVEPVASI 437
K ++ D LV+GTS V P A I
Sbjct: 171 EELDRAFKLAEKADAVLVVGTSGLVYPAAYI 201

sp|P53688|HST4_YEAST HST4 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 4) >gi|1077540|pir||S52699
hypothetical protein YDR191w - yeast (Saccharomyces cerevisiae) >gi|755785|emb|CAA88705| (248784) unknown
[Saccharomyces cerevisiae]

Length = 370

Score = 76.5 bits (185), Expect = 5e-13
Identities = 70/244 (28%), Positives = 119/244 (48%), Gaps = 32/244 (13%)

Query: 231 LSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQL---SKLNLSDPQKVFDLQTFMREGR 286
L+ +K+++VV+GAGIS + GIPDFRS +G+++ + S +L D +V+ D ++ +
Sbjct: 89 LNYSKRMVVSGAGISVAAGIPDFRSSEGIFSTVNGGSGKDLFDYNRVYGDMSMSLKFNQ 148

Query: 287 LFYTIAHLVLPPDGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQRAGLKSEKL----- 340
L ++ L + + + H L +LLR YTQNID L+ + S +
Sbjct: 149 LMVSLFR--LSKNQPTKFHEMLNEFARDGRLRLYQTQNIDGLDTQLPHLSTNVPLAKPI 206

Query: 341 ---VQCHGSFAKAKCVSCQGI-----FAGEKIYNHIRRKQVPRCAICWKN---TKQAP 387
VQ HGS +C C I F + ++ R + +P C C + K A
Sbjct: 207 PSTVQLHGSIKHMECNKCLNPKPDFPELFCKCDDKFDS-RTEIIPSCPQCCEYEYETVRKMA 265

Query: 388 IH---FGAIKPTITFFGEDLPER--FHTLMDKDL-QQIDLFLVIGTSLKVEPVASI 441
+ G ++P + E PE + + DL ++ID +++GTSLK+ V +I +
Sbjct: 266 LRSTGVGKLRLPRVILYNEVHPEGDFIGEIANNDLKKRIDCOLIIVGTSKLIPGVKNICRQF 325

Query: 442 PYKV 445
KV
Sbjct: 326 AAKV 329

[gb|AAD42226.1|AF159133_1](#) (AF159133) SIR2-like protein [Oryza sativa subsp. indica]
Length = 483

Score = 76.5 bits (185), Expect = 5e-13
Identities = 63/216 (29%), Positives = 98/216 (45%), Gaps = 29/216 (13%)

Query: 223 KLPDLISDLSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFM 282
K+ +L + +K++V TGA ISTS GIPDFR KG++ L+ P Q
Sbjct: 33 KIEELAVMVRESKHLVVFTGASISTSSGIPDFRGPKGVWT-LQRSGKGVPAGATLPFQ--- 88

Query: 283 REGRLFYTIAHLVLPPDGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQRAGLKSEKLVQ 342
R+ T+ H+ L L+ +L +QN+D+L R+GL EKL +
Sbjct: 89 ---RAVPTLTTHMALVE-----LEKTGRLKFVIISQNVDSLHRSGLPREKLAE 132

Query: 343 CHGSFAKAKCVSCQGIFAGEKIYNHIRRKQVPRCAICWKNTKQAPIHFGA-IKPTITFFG 401
HG+ K C SC+ + + I K PR + + + GA +K T+ +
Sbjct: 133 LHGNNSFKEICPSCKKEYLRFETIETIGLKDTPR-----RCSDKNCARLKDVTLDWE 184

Query: 402 EDLPERFHTLMDKDLQQIDLFLVIGTSLKVEPVASI 437
+ LP + Q DL L +GTSL++ P ++
Sbjct: 185 DALPPEEMDAAKEQCQTADLVLCLGTSLQITPACNM 220

[dbj|BAA30044|](#) (AP000004) 249aa long hypothetical protein [Pyrococcus horikoshii]
Length = 249

Score = 76.1 bits (184), Expect = 6e-13
Identities = 60/212 (28%), Positives = 99/212 (46%), Gaps = 24/212 (11%)

Query: 231 LSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFY 290
L+ +K++ TGAGIS GIP FR GL+ + L+ P + F R +L +
Sbjct: 9 LASSKNVIAFTGAGISAESGIPFRGKDGLWKKYRPEELATP-----EAERNPKLVWD 62

Query: 291 IAHLVLPP--DGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQRAGLKSEKLVQCHGSFA 348
+ K+ H L L+ L TQN+D+L + AG K+ L++ HG+
Sbjct: 63 FYKWRIKILKAKPNPAHYALVELEMGILKAVITQNVDDLHREAGTKN--LIELHGNIF 120

Query: 349 KAKCVSC---QGIFAGEKIYNHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLP 405
+ +C SC + + +I + I + +P+C C ++P + +FGE LP
Sbjct: 121 RVRCTSCEFREHLKESGRI-DEILSEDLPKCPKCG-----SLLRPDVVWFGEPLP 169

Query: 406 ERFHTLMDKDLQQIDLFLVIGTSLKVEPVASI 437
+ K ++ D+ +V+GTS V P A I
Sbjct: 170 SKELNEAFKLAKEDVVIVVGGTGLVYPAAI 201

[gb|AAD15478|](#) (AC006930) R33423_1 [Homo sapiens]
Length = 377

Score = 74.5 bits (180), Expect = 2e-12
Identities = 68/272 (25%), Positives = 121/272 (44%), Gaps = 38/272 (13%)

Query: 233 RAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFY 292
++ ++ TGAGIST+ GIPDFR G++ + + L+ FD T R T
Sbjct: 43 QSSSVVFHTGAGISTASGIPDFRGPHGVWT-MEERGLAPK---FD--TTFESARPTQT-- 94

Query: 293 HLVLPPDGKFSLLHAFLKLLQDKHKLRLRNYTQNIDNLEQRAGLKSEKLVQCHGSFAKAKC 352
H+ L + LL + +QN+D L R+G +KL + HG+ +C
Sbjct: 95 HMALVQLERVGLLRFLV-----SQNVDGLHVRSGFPRDKLAEIHGNMFVEEC 141

Query: 353 VSCQGIFAGEKIYNHIRRKQVPRCAICWK-----NTKQAPIHFGAIKPTI 397
C+ + + + K R K ++ Q P G ++ TI
Sbjct: 142 AKCKTQYVRTVVGTMGLKATGRLCTVAKARGLRACRGGEAPEDSPQLPHCRGELRTI 201

Query: 398 TFFGEDLPERFHTLMDKDLQQIDFLVLVIGTSKLVEPVASIIERVPYKVPK-ILINKDPIP 456
+ + LP+R L D+ + DL + +GTSL++ P ++ + + +++N P
Sbjct: 202 LDWEDSLPDRDLALADEASRNADLSITLGTSLQIRPSGNLPLATKRRGGRLVIVNLQPTK 261

Query: 457 -NRGFNLQLLGLCDDAVSYLCKCLKWDIPHAD 487
+R +L++ G D+ ++ L K L +IP D
Sbjct: 262 HDRHADLRIHGYDEVMTRLMKHLGLEIPAWD 293

emb|CAB56682.1| (AL121596) putative SIR2-like regulatory protein [Streptomyces coelicolor A3(2)]
Length = 299

Score = 70.6 bits (170), Expect = 3e-11
Identities = 67/261 (25%), Positives = 108/261 (40%), Gaps = 58/261 (22%)

Query: 228 ISDLSRAKKIMVVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRL 287
++D RA ++V++GAGIST GIPD+R G L+ P D R
Sbjct: 25 VADALRAGGVVLSGAGISTESGIPDYRGEggg----SLSRHTPMTYQDFTAHPEARRR 78

Query: 288 FYTIAHL-----VLPPDGKFSLLHAFKLQLQDKHKLLRN-YTQNIDNLEQRAGLKSEKL 340
++ +HL P+ + AF +H LL TQN+D L Q AG SE +
Sbjct: 79 YWARSHLGWRTRFGGRARPNAGHRSVAAF----GRHGLLTGVTQNVDGLHQAAAG--SEGv 131

Query: 341 VQCHGSFAKAKCVSCQGIFAGEKIYNNHIRRK-----QV 373
V+ HGS + C+SC + ++ + +V
Sbjct: 132 VELHGSLLDRVVCCLSGVLPSPRELARRLEEANAGFSPVAAGINPDGDADLTDEQVGDFRV 191

Query: 374 PRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTLMDKDLQQIDFLVLVIGTSKLKV-E 432
CA+C G +KP + FFGE++P R + ++ LV+G+SL V
Sbjct: 192 VPCAVCG-----GVLKPDVVFGENVPPRRVEHCRELVRGASSLLVGSSLTVMS 241

Query: 433 PVASIIERVPYKVPKILINKD 453
+ + + P +++N+D
Sbjct: 242 GLRFVRQAAEAGKPVLIVNRD 262

gb|AAD40852.1|AF083109_1 (AF083109) sirtuin type 4 [Homo sapiens]
Length = 314

Score = 69.5 bits (167), Expect = 6e-11
Identities = 73/270 (27%), Positives = 114/270 (42%), Gaps = 61/270 (22%)

Query: 225 PDLISDLR---AKKIMVVVTGAGISTSLGIPDFRSFK-GLYNQLSKLNLSDPQKVFDLQ 279
P+ + +L R +K+++V+TGAGIST GIPD+RS K GLY + + +
Sbjct: 41 PEVKELQRFITLSKRLLVMGAGISTESGIPDYRSEKVGLYARTDRRPIQHGD----- 94

Query: 280 TFMRREG--RLFYTIAHLVLPDGKFSL---LHAFLKLLQDKHKLLRN-YTQNIDNLEQR 332
F+R R Y + V P +FS H L + KL TQN+D L +
Sbjct: 95 -FVRSAPIRQRYWARNFVGWP---QFSSHQPNAPAHWALSTWEKLGKLYWLVTQNVDALHTK 151

Query: 333 AGLKSEKLVQCHGSFAKAKCVSC-----QGIFAGEKIY--- 365
AG S +L + HG + C+ C G+ ++
Sbjct: 152 AG---SRRTELHGCMDRVLCLCDGEQTPRGVQLQERFQVLNPTWSAEAHGLAPGDGVFLSE 209

Query: 366 NHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTLMDKDLQQIDFLVVI 425
+R QVP C C G +KP + FFG+ + + K +++ D LV+
Sbjct: 210 EQVRSFQVPTCVQCG-----GHLKPDVVFQDTVNPDKVDFVHKRVKEADSLLVV 259

Query: 426 GTSLKV-EPVASIIERVPYKVPKILINKD 454
G+SL+V I+ K+P ++N P
Sbjct: 260 GSSLQVYSGYRFILTAWEKKLPIAILNIGP 289

gb|AAC70895| (AF006830) unknown [Actinobacillus actinomycetemcomitans]
Length = 208

Score = 69.1 bits (166), Expect = 8e-11
Identities = 68/224 (30%), Positives = 104/224 (46%), Gaps = 26/224 (11%)

Query: 238 MVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIAHLVLP 297
+V++GAGIS GIP +R+ GL+ ++ P+ LQ ++ FY
Sbjct: 6 VVLSGAGISAESGIPTYRAEDGLWAGHKIEDVCTPEA---LQRNRKQVLAFYNERRRNCA 62

Query: 298 PDGKFSLLHAFKLQLQDKHKLLRN-YTQNIDNLEQRAGLKSEKLVQCHGSFAKAKCVSCQG 357
+ K + H L L+ + + TQN++L +RAG S ++ HG KA+
Sbjct: 63 -EAKPNAAHKVLVELERSYN-QIITQNVEDLHERAG---STNVLHLHGELETKAR----S 113

Query: 358 IFAGEKIHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTLMDKDLQ 417
F + I + + V N K H ++P I FFGE +P +D +
Sbjct: 114 SFDPDYIVPCMGSQSV-----NDKDPNGH--PMRPHIVFFGESVPV-LEPAIDL-VS 161

Query: 418 QIDLFLVIGTSKLVEPVASIIERVPYKVPKILINKDPIPQRGFN 461
Q D+ LVIGTSL+V P ++ P LI DP PN GFN
Sbjct: 162 QADIVLVIGTSQVYPANGLVNEAPKNAQIYLI--DPNPNTGFn 203

emb|CAB09010| (Z95584) hypothetical protein Rv1151c [Mycobacterium tuberculosis]

Length = 237

Score = 67.5 bits (162), Expect = 2e-10
Identities = 68/235 (28%), Positives = 110/235 (45%), Gaps = 36/235 (15%)

Query: 236 KIMVVTGAGISTSLGIPDFRSFK-GLYNQLSKLNLS-----DPQKVFDLQTFMREGRL 287
++ V++GAGIS G+P FR K GL+ + LS +P++V+ +
Sbjct: 2 RVALSGAGISAESGVPTFRDDKNGLWARFDPYELSSTQGWLRNPERVWGWLWRH--- 57

Query: 288 FYTIAHLVLPPDGKFSLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLKSEKLVQCHGSF 347
Y+A+ V P DG H + QD H + TQN+D+L +RAG S + HGS
Sbjct: 58 -YLVAN-VEPNNDG----HRAIAAWQD-HAEVSITQNVDLHERAG--SGAVHHLHGSL 107

Query: 348 AKAKVSCQGIFAGEKEIYHNIRRQVPRCAICWKNTKQAPI--HFGAIKPTITFFGEDLP 405
+ +C C G+ + + ++P AI + P+ G I+P I +FGE LP
Sbjct: 108 FEFRCARC-GVPTYDAL----PEMPPEPAI---EVEPPVCDCGGLIRPDIVWFGEPPLP 156

Query: 406 ERFHTLMDKDLQQIDLFLVIGTSLKVEPVASIIERVPYKVKIL-INKDPIPNRG 459
E + D+ +V+GTS V P A + + + ++ +N +P P G
Sbjct: 157 EEPWRSAVEATGSADVMVVVGTSIAIVPAAGLPLALARGTAVIEVNPEPTPLSG 211

emb|CAA90546.1| (Z50177) similar to SIR; cDNA EST yk300f10.3 comes from this gene;
cDNA EST yk522h8.3 comes from this gene [Caenorhabditis elegans]
Length = 287

Score = 66.3 bits (159), Expect = 5e-10
Identities = 63/244 (25%), Positives = 102/244 (40%), Gaps = 55/244 (22%)

Query: 224 LPDLISDLRSRAKKIMVVTGAGISTSLGIPDFRSFK-GLYNQLSKLNLSDPQKVFDLQTFM 282
L IS + K++V++GAGIST GIPD+RS GLY +++ K Q +M
Sbjct: 17 LKKFISLIGTVDKLLVISGAGISTESGIPDYRSKDVGLYARIA-----HKPIYFQDYM 69

Query: 283 REGRL---FYTIAHLVLPPDGKF--SLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLKS 337
R R +++ L P G+ ++ H L + + TQN+D L +AG S
Sbjct: 70 RSNRCRQRYWSRNFLAWPRFGQAAPNINHYALSWEASDRFQWLITQNVDGLHLKAG--S 127

Query: 338 EKLVQCHGSFAKAKCVSCQGIFAGEKEIYHN----- 368
+ + + HGS + KC +C I + + +
Sbjct: 128 KMVTELHGSALQVKCTTCDYIESRQTYQDRLDYANPGFKEEHVAPGELAPDGDIIPLGT 187

Query: 369 -RRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPFRHTLMDKDLQQIDLFLVIGT 427
+ Q+P C C G +K +TFFGE++ + + + D L +GT
Sbjct: 188 EKGFBQIPECPSCG-----GLMKTDVTFFGENVNMDKVNFCYEKVNEDGILSLGT 237

Query: 428 SLKV 431
SL V
Sbjct: 238 SLAV 241

gb|AAB95634| (AC003982) unknown function; 60% similar to Z50177 (PID:g927403)
(PID:g927402) [Homo sapiens]
Length = 326

Score = 64.0 bits (153), Expect = 3e-09
Identities = 74/284 (26%), Positives = 114/284 (40%), Gaps = 77/284 (27%)

Query: 225 PDLISDLR---AKKIMVVTGAGISTSLGIPDFRSFK-GLYNQLSKLNLSDPQKVFDLQ 279
P+ + +L R +K++V+TGAGIST GIPD+RS K GLY + + +
Sbjct: 41 PEKVKELQRFITLSKRLVMTGAGISTESGIPDYRSEKVGLYARTDRRPIQHGD---- 94

Query: 280 TFMREG--RLFYTIAHLVLPPDGKFLS----LHAFLKLLQDKHKLLRNYTQNIDNLEQR 332
F+R R Y + V P +FS H L + KL TQN+D L +
Sbjct: 95 -FVRSAPIRQRYWARNFVGWP--QFSSHQPNAHWALESWEEKLGKLYWLVTQNVDALHTK 151

Query: 333 AGLKSEKLVQCHGSFAKAKCVSCQGIFAGEKEIY----- 365
AG S +L + HG +A C +F G ++
Sbjct: 152 AG--SRRTELHGCMRDAYC--SVSVFLGSRVLCLDCGEQTPRGVLQERFQVLNPTWSAE 207

Query: 366 -----NHIRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPFRHTL 411
+R QVP C C G +KP + FFG+ +
Sbjct: 208 AHGLAPDGDFVLEEQVRSFQVPTCVQCG-----GHLKPDVVFQGDTVNPDKVDF 257

Query: 412 MDKDLQQIDLFLVIGTSLKV-EPVASIIERVPYKVKILINKDP 454
+ K +++ D LV+G+SL+V I+ K+P ++N P
Sbjct: 258 VHKLKRVEADSSLVVGSSLQVYSGYRFILTAWEKKLPIAIALNIGP 301

gi|4155790| (AE001545) putative [Helicobacter pylori J99]
Length = 234

Score = 63.6 bits (152), Expect = 3e-09
Identities = 57/213 (26%), Positives = 94/213 (43%), Gaps = 44/213 (20%)

Query: 235 KKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLS-----DPQKVFDLQTFMREGRL 287
K +++++GAGIS GI FR GL+ + ++ +PQKV D R +L
Sbjct: 2 KNLVLILSGAGISAESGIKTFRDAGGLWEGHDIIMEVASPYGWKKNPQKVLFYN-QRRRQL 60

Query: 288 FYTIAHLVLPDPDKFSSLHAFKLQLQDKHKLLRNYTQNIDNLEQRAGLKSEKLVQCHGSF 347
F V P +L +KH + TQN+D+L +RAG S +++ HG
Sbjct: 61 FE----VYPNKAHKALABEL-----EKHYQVNIIITQNVDDLHERAG--SSRILHLHGEL 107

Query: 348 AKAKCVSCQGIFAGEKEIYNHIRRQVPRCAICWK---NTKQAPIHFGAIKPTITFFGEDL 404
+R ++ P W+ N ++P I +FGE++
Sbjct: 108 LS-----VRSEKDPNLVYRWEKDLNLGDLAQDKAQLRPDIVWFGEVV 149

Query: 405 PERFHTELMKDQLQQIDLFLVIGTSLKVEPVASI 437
P + ++Q+ L ++IGTSL+V P AS+
Sbjct: 150 PLLKEAV--SLVKQVHLLIIIGTSLQVYPAASL 180

[emb|CAA90547.1|](#) (Z50177) similar to SIR [Caenorhabditis elegans]
Length = 287

Score = 60.1 bits (143), Expect = 4e-08
Identities = 56/229 (24%), Positives = 97/229 (41%), Gaps = 49/229 (21%)

Query: 236 KIMVVTGAGISTSLGIPDFRSFK-GLYNQLSKLNLSDPQKVFDLQTFMREGRFLFYIAHL 294
K+++TGAGIST GIPD+RS GLY + + +P D + + + +L
Sbjct: 29 KLLIITGAGISTESGIPDYRSKDVGLYTKTA---LEPIYFQDFMKSKKCRQRYWSRSYL 84

Query: 295 VLPPDGKF--SLLHAFLKLLQDKHKLLRNYTQNIDNLEQRAGLKSEKLVQCHGSFAKAC 352
P + + H L + +K TQN+D L +AG S+ + HG+ + KC
Sbjct: 85 NWPRFAQALPNFNHYALSWEAANKFHWLITQNVDGLHLKAG--SKMITELHGNALQVKC 142

Query: 353 VSCQGIFAGEKEIYNHIRRK-----QVPRCAICWKN 382
SC+ I + + + +P C C
Sbjct: 143 TSCEYIETRQTYQDRLNANPGFKEQFVSPGQQELDACTLPLGSEQGFKIPECLNCG-- 200

Query: 383 TKQAPIHFGAIKPTITFFGEDLPERFHTELMKDQLQQIDLFLVIGTSLKV 431
G +K +T FGE+L + K + + + L +GTSL+V
Sbjct: 201 -----GLMKTDVTLFGENLNNTDKIKVCGKKVNECNGVLTGTSLEV 241

[gi|2996605|](#) (U89687) putative nicotinic acid mononucleotide:5,
6-dimethylbenzimidazole(DMB)phosphoribosyltransferase
[Salmonella typhimurium]
Length = 237

Score = 60.1 bits (143), Expect = 4e-08
Identities = 61/214 (28%), Positives = 98/214 (45%), Gaps = 40/214 (18%)

Query: 236 KIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFD---LQTF-----MRE 284
++V+TGAGIS GI FR+ GL+ + +++ P+ +QTF +++
Sbjct: 6 RVLVLTGAGISAESGIRTFAADGLWEEHRVEDVATPEGFARNPGLVQTFYNARRQQLQQ 65

Query: 285 GRLFYTIAHLVLPDPDGKFLQDKHLLRNYTQNIDNLEQRAGLKSEKLVQCH 344
+ AHL L + K L AFL + TQNIDNL +RAG + ++Q H
Sbjct: 66 PEIQPNAAHAL-ANLKKRLAIAFLV-----TQNIDNLHERAG--NRNIIQMH 111

Query: 345 GSFAKAKCVSCQGIFAGEKEIYNHIRRQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDL 404
G K +C +G+ + +C C Q P ++P + +FGE +
Sbjct: 112 GELLKVRCQS----SGQILEWNGDVPMPEDKCHCC----QFP---APLRPHVVWFGE-M 157

Query: 405 PERFHTELMKDQLQQIDLFLVIGTSLKVEPVASII 438
P + L D+F+ IGTS V P A +
Sbjct: 158 PLGMDEIY-MALSMADIFIAIGTSGHVYPAAGFV 190

[gi|1787364|](#) (AE000212) putative nicotinic acid
mononucleotide:5,6-dimethylbenzimidazole (DMB)
phosphoribosyltransferase [Escherichia coli]
>gi|4062692|dbj|BA35940| (D90747) ORF_ID:o238#9
[Escherichia coli]
Length = 279

Score = 58.6 bits (139), Expect = 1e-07
Identities = 59/214 (27%), Positives = 96/214 (44%), Gaps = 22/214 (10%)

Query: 227 LISDLSSRAKKIMVVTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGR 286
++ + +V+TGAGIS GI FR+ GL+ + +++ P+ FD + +
Sbjct: 33 VVPEAMEKPRVLVTGAGISAESGIRTFAADGLWEEHRVEDVATPEG-FDRDPELVQA- 90

Query: 287 LFYTIAHLVLPDPDGKFLQDKHLLRNYTQNIDNLEQRAGLKSEKLVQCH 344
FY L P+ + + H L LQD TQNIDNL +RAG + ++ H
Sbjct: 91 -FYNARRRQLQQPEIOPNAAHLALAKLQDALGDRFLVTQNIIDNLHERAG--NTNVIHMH 147

Query: 345 GSFAKAKCVSCQGIFAGEKEIYNHIRRQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDL 404
G K +C +G+ + +C C Q P ++P + +FGE +
Sbjct: 148 GELLKVRCQS----SGQVLDWTGDPEDKCHCC----QFP---APLRPHVVWFGE-M 193

Query: 405 PERFHTELMKDQLQQIDLFLVIGTSLKVEPVASII 438
P + L D+F+ IGTS V P A +
Sbjct: 194 PLGMDEIY-MALSMADIFIAIGTSGHVYPAAGFV 226

[gi|1943780|](#) (U97193) similar to S. cerevisiae SIR2 (SP:P06700) and mouse hepatoma

derived growth factor HDGF (NID:g945418) [Caenorhabditis elegans]
 Length = 1095

Score = 57.8 bits (137), Expect = 2e-07
 Identities = 49/203 (24%), Positives = 83/203 (40%), Gaps = 24/203 (11%)

Query: 235 KKIMVVGTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTI AHL 294
 K I V+ GAG+ST +PDFR +G++ T EG+ +
 Sbjct: 852 KPIFLIGAGVSTGSKLPFRGKQGVW-----TLQAEKGKAEGVDFQ 893

Query: 295 VLPPDGKFSLLHAFLKLLQDKHKLLRNNTQNIDNLEQRAGLKSEKLVQCHGSFAAKCVS 354
 V P + H + L + TQN+D L+++ G+ E L++ HG+ C S
 Sbjct: 894 VARP----GVSHKSILALHKAGYIKTIITQNVDGLDRKVGIPVEDLIEVHGNLFLEV CQS 949

Query: 355 CCGIFAGEKEIYNIHRRKQVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTLM DK 414
 C + E+I + P C N + G ++ + ++ + K
 Sbjct: 950 CFSEYVREEIVMSV--GLCPTGRNCEGNKRTGRCSR GKL RDATLDWDTEISLNHLD RIRK 1007

Query: 415 DLQQIDLFLVIGTSLKVEPVASI 437
 +Q L IGTSL++ P+ S+
 Sbjct: 1008 AWKQTSHLLCIGTSLEIIPMGSL 1030

[emb|CAA22773|](#) (AL035206) putative SIR2 family transcriptional regulator
 [Streptomyces coelicolor]
 Length = 190

Score = 52.3 bits (123), Expect = 9e-06
 Identities = 37/140 (26%), Positives = 59/140 (41%), Gaps = 12/140 (8%)

Query: 319 LRNYTQNIDNLEQRAGLKSEKLVQCHGSFAAKCVSCQGIFAGEKEIYNIHRR-KQVPRCA 377
 +R TQN+D L Q AG+ + K+++ HG+ C C + I + P C
 Sbjct: 36 VRVLTQNVDGLHQLAGVSARKVLELHGTA RD C VCTGCGARGPMADVLARIEAGEDDPPCL 95

Query: 378 ICWKNTKQAPIHFGAIKPTITFFGEDLPERFHTLMKD L QQIDLFLVIGTSLKVEPVASI 437
 C G +K FGE L + +F+ +GTSL+VEP A +
 Sbjct: 96 DCG-----GVLKTATVMFGERLDPVVLGEAAAISKACQVFVAVGTSQV EP AAGL 145

Query: 438 IE-RVPYKVPKILINKDPIP 456
 V + +++N +P P
 Sbjct: 146 ARVAVEH GARL VVVNAEPTP 165

[emb|CAB55543.1|](#) (AL117324) possible sirtuin [Leishmania major]
 Length = 320

Score = 47.6 bits (111), Expect = 2e-04
 Identities = 57/242 (23%), Positives = 88/242 (35%), Gaps = 50/242 (20%)

Query: 233 RAKKIMVVGTGAGISTSLGIPDFRSFKGLYNQLSKLNLSDPQKVFDLQTFMREGRLFY 289
 R + +V+TGAG ST GIPD+R G Y++ + L+ Q FMR E R ++
 Sbjct: 19 RGRGCVVL TGAGC STESGIPDYRGPNQYHRADFVLLT-----FQKFMRDDNEKRRYW 71

Query: 290 TIAHLVLPP--DGKFSLLHAFLKLLQDKHKLLRNNTQNIDNLEQR A-----GLKSEK--- 339
 + L + H L+ + TQN+D L A G E+
 Sbjct: 72 ARSMLGYSTMCGASCNAAHMALQAFTKSGAVA HILTQNVDGLHHLATYGGVGDAEEEHY 131

Query: 340 -----LVQCHGSFAAKCVSCQGIFAGEKEIYNIHRR----- 371
 L + HG+ C SC ++ +R +
 Sbjct: 132 KYTTSDAPLKE LHGNIHNVICTSCGFFMPRARLQREL RERNP GFYEQYGADVS RTRPDGD 191

Query: 372 -QVPRCAICWKNTKQAPIHFGAIKPTITFFGEDLPERF-HTLMDKDLQQIDLFLVIGTSL 429
 P A+ + P G KP + FGE++P+ M + L +GTSL
 Sbjct: 192 YSATPEAVNAMHLMCPRCNFFKPHVVLFGENVPKP IVEATMSLVRDKASCLLC LGTSL 251

Query: 430 KV 431
 +V
 Sbjct: 252 QV 253

[gb|AAD08305.1|](#) (AE000631) conserved hypothetical protein [Helicobacter pylori 26695]
 Length = 205

Score = 45.3 bits (105), Expect = 0.001
 Identities = 34/127 (26%), Positives = 57/127 (44%), Gaps = 25/127 (19%)

Query: 314 DHKLLRNNTQNIDNLEQRAGLKSEKLVQCHGSFAAKCVSCQGIFAGEKEIYNIHRRKQV 373
 +KH + TQN+D+L +RAG S +++ HG +R ++
 Sbjct: 52 EKHYQVNII ITQNVDLHERAG--SSRILHLHGE L LLS-----VRSEKD 91

Query: 374 PRCAICWK----NTKQAPIHFGAIKPTITFFGEDLPERFHTLMKD L QQIDLFLVIGTSLK 430
 P W+ N ++P I +FGE +P + ++Q L ++IGTSL+
 Sbjct: 92 PNLVYRWEKDLNLGDLAKDKSQLRPDIWVFG EAVPLLKEAI--SLVKQAHLLII GTSLQ 149

Query: 431 VEPVASI 437
 V P AS+
 Sbjct: 150 VYPAA SL 156

[gi|3548790](#) (AC005620) R33590_2, partial CDS [Homo sapiens]

Length = 121

Score = 35.2 bits (79), Expect = 1.3

Identities = 17/57 (29%), Positives = 33/57 (57%)

Query: 381 KNTKQAPIHFGAIKPTITFFGEDLPERFHTLMDKDLQQIDLFVLVIGTSLKVEPVASI 437
+++ Q P G ++ TI + + LP+R L D+ + DL + +GTSL++ P ++
Sbjct: 39 EDSPQLPHCRGELRDTILDWEDSLPDRDLALADEASRNADLSITLGTSLQIRPSGNL 95

[sp|P44781|HEPA_HAEIN](#) RNA POLYMERASE ASSOCIATED PROTEIN HOMOLOG (ATP-DEPENDENT HELICASE HEPA) >gi|1073887|pir||H64081 ATP-dependent helicase (hepA) homolog - Haemophilus influenzae (strain Rd KW20) >gi|1573610 (U32744) ATP-dependent helicase (hepA) [Haemophilus influenzae Rd]
Length = 923

Score = 34.4 bits (77), Expect = 2.2

Identities = 27/95 (28%), Positives = 46/95 (48%), Gaps = 7/95 (7%)

Query: 259 GLYNQLSKLNLSDPQKVFDLQTFMREGRLFYTIHLV--LPPDGKFSLLH---AFLKLL 312
G + ++L D P++ FD QTF++E + + + V L + S + + L L
Sbjct: 318 GQESHFARLRLLDPERFFDYQTFVKEQEHYQPVVNAVESLLANKALSAVEKNHISDLLLE 377

Query: 313 QDKHKLLRNYTQNIDNLEQRAGLK-SEKLVQCHGS 346
QD L + N D +QRA + + L+ HG+
Sbjct: 378 QDVEPLFKAIASNNDEEQQRARQELIQALIDRHGT 412

[emb|CAB59689.1|](#) (AL132675) zinc-finger protein [Schizosaccharomyces pombe]
Length = 374

Score = 34.0 bits (76), Expect = 2.8

Identities = 18/58 (31%), Positives = 26/58 (44%), Gaps = 2/58 (3%)

Query: 329 LEQRAGLKSEKLVQCHGSFAKAKCVSCQGIFAGEKIYNHIRRKVPRCAICWKNTKQA 386
L+ EK++ S CV +G ++ NHIR VP C+IC + K A
Sbjct: 161 LQNHVNRAHEKIISY--SCPHECSVGHEGFEKWSQLQNHIREAHVPSCSICGRQFKTA 216

[sp|P32863|RA54_YEAST](#) DNA REPAIR AND RECOMBINATION PROTEIN RAD54 >gi|83449|pir||JH0440
RAD54 protein - yeast (Saccharomyces cerevisiae)
>gi|172343 (M63232) recombination and repair protein [Saccharomyces cerevisiae] >gi|728692|emb|CAA88534| (Z48618) RAD54 [Saccharomyces cerevisiae]
>gi|1322760|emb|CAA96875| (Z72685) ORF YGL163c [Saccharomyces cerevisiae]
Length = 898

Score = 32.8 bits (73), Expect = 6.3

Identities = 36/151 (23%), Positives = 63/151 (40%), Gaps = 33/151 (21%)

Query: 215 INMTPFKYKLPLDISDLSRAKKIMV-VTGAGISTSLGI-----PDFRSFKGLYNQLSK 266
+N+ P + +L + + KK++ V G+ ++GI P+ +F+ ++
Sbjct: 573 VNLKPLQNEYNKLIKSRREVKKVVKGVGGSQLRAIGILKKLCNHPNLLNFEDEFDDDEDD 632

Query: 267 LNLSDP----QKVFDLQTFMREGRLFYTI AHLVLPPDGKFSLLHAFLKLLQ---DKHK 317
L L D K D+QT KFS+L FL ++ DK
Sbjct: 633 LELPDYNNMPGSKARDVQTKY-----SAKFSILERFLHKIKTESDDKIV 676

Query: 318 LLRNYTQNIDNLEQRAGLKSEKLVQCHGSFA 348

L+ NYTQ +D +E+ K V+ G+ +
Sbjct: 677 LISNYTQTLDSLIEKMCRYKHYSAVRLDGTMS 707

CPU time: 51.64 user secs. 0.95 sys. secs 52.59 total secs.

Database: Non-redundant GenBank CDS
translations+PDB+SwissProt+SPupdate+PIR

Posted date: Nov 7, 1999 2:25 PM

Number of letters in database: 129,676,735

Number of sequences in database: 422,855

Lambda K H
0.320 0.138 0.406

Gapped
Lambda K H
0.270 0.0470 0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 116249722
Number of Sequences: 422855
Number of extensions: 4690247

```
Number of successful extensions: 10923
Number of sequences better than 10.0: 51
Number of HSP's better than 10.0 without gapping: 45
Number of HSP's successfully gapped in prelim test: 6
Number of HSP's that attempted gapping in prelim test: 10758
Number of HSP's gapped (non-prelim): 59
length of query: 515
length of database: 129676735
effective HSP length: 55
effective length of query: 460
effective length of database: 106419710
effective search space: 48953066600
effective search space used: 48953066600
T: 11
A: 40
X1: 16 ( 7.4 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 41 (21.8 bits)
S2: 72 (32.5 bits)
```

How *Candida albicans* switches phenotype - and back again

An essential gene for phenotypic switching in *C. albicans* is similar to SIR2, a gene-silencing gene

S. cerevisiae SIR2	[260]-	TGAGVSTSLGIPDFRS	-[66]-	TQNID	-[24]-	CV--TC-[20]-CPYCY	-[162]
<i>Candida albicans</i>	[240]-	TGAGISTSLGIPDFRS	-[66]-	TQNID	-[24]-	CV--SC-[20]-CAICW	-[135]
<i>Trypanosoma brucei</i>	[35]-	VGAGISVAAGIPDFRS	-[69]-	TQNID	-[24]-	CV--DC-[20]-CNQCG	-[173]
Human	[45]-	VGAGISTSAGIPDFRS	-[67]-	TQNID	-[24]-	CVSASC-[20]-CEDCQ	-[164]
<i>D. melanogaster</i>	[225]-	TGAGVSVSCGIPDFRS	-[70]-	TQNID	-[22]-	CT--KC-[20]-CPQCQ	-[456]
<i>Staph. aureus</i>	[21]-	TGAGVSVASGVPDFRS	-[66]-	TQNID	-[22]-	CN--VC-[16]-CDNCG	-[88]
<i>Thermotoga maritima</i>	[19]-	TGAGISTPSGIPDFRG	-[61]-	TQNID	-[22]-	CV--RC-[20]-CDDCN	-[94]

The *Candida albicans* SIR2 conserved core (yellow shading) matches many proteins in the sequence database, originating from humans to bacteria. A range of these proteins is aligned above. Two highly conserved motifs (in green and blue) are found within this conserved core domain and are characteristic for SIR2 proteins. Each is essential for SIR2 silencing function [1], although their exact role remains a mystery. Also shown is a pattern of four conserved cysteine residues; these are thought to be make a zinc finger DNA-binding motif. The numbers in parentheses represent the number of amino acids found at each end of the conserved core and in between the motifs of the conserved core. To view the sequence records from which this alignment was made, click on the organisms name.

Trypanosoma brucei is unicellular eukaryotic parasite that causes sleeping sickness. *D. melanogaster* is a fruit fly - a model organism sequenced for comparative purposes as a part of the Human Genome Project. *Staphylococcus aureus* is a well-studied bacterium; the protein used in this alignment is a conceptual translation of a gene, *lacR*, originally isolated as a repressor of the lactose operon. *Thermotoga maritima* is an extreme thermophilic archaeabacterium that lives near deep-sea hydrothermal vents. Its SIR2-like protein is a conceptual translation from a section of the complete genome sequence.

[Back to BLAST result](#)

The *Candida albicans* SIR2 protein was used to search the non-redundant protein sequence database using the PSI-BLAST program [3] with standard parameters. Sequences included in the multiple alignment of the SIR2 conserved core were selected from output from the first iteration. The multiple sequence alignment was constructed using ClustalW [4].

[1] Sherman, J.M., Stone, E.M., Freeman-Cook, L.L., Brachmann, C.B., Boeke, J.D. and Pillus, L. (1999) The conserved core of a human SIR2 homologue functions in yeast silencing. *Mol. Biol. Cell* 10, 3045-3059

[2] Perez-Martin, J., Uria, J.A. and Johnson, A.D. (1999) Phenotypic switching in *Candida albicans* is controlled by a SIR2 gene. *EMBO J.* 18, 2580-2592

[3] Altschul, S. F. et al. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* 25, 3389-402

[4] Higgins, D. G., Thompson, J. D. and Gibson, T. J. (1996) Using CLUSTAL for multiple sequence alignments. *Methods Enzymol.* 266, 383-402